

; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-902-188A-7

Query Match 96.5%; Score 2613; DB 9; Length 485;
Best Local Similarity 95.5%; Pred. No. 7e-234;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDYLDFGEFNOGKTIRTKYGTNRQLQAQAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Db 61 YDYLDFGEFNOGKTIRTKYGTNRQLQAQAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Qy 121 EVNPNRNQVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQVSGEYTIETAWTRDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RDKGKWDWEVDTENGNYDYLAMVADIMDHPPEVNNELRNWGVYTTNLGLDGFRIIDAVKH 240
Db 181 RDKGKWDWEVDTENGNYDYLAMVADIMDHPPEVNNELRNWGVYTTNLGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAFKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAFKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300
Qy 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Db 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Qy 361 QGYPVFGDYGIPTGHPVPAKSKIDPILKQYAYGRNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVFGDYGIPTGHPVPAKSKIDPILKQYAYGRNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGNFVSGSVS 480
Db 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGNFVSGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485
RESULT 11
US-09-925-576C-13
; Sequence 13, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjørn Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: bacillus sp. 707
US-09-925-576C-13
Query Match 96.5%; Score 2613; DB 10; Length 485;
Best Local Similarity 95.5%; Pred. No. 7e-234;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDYLDFGEFNOGKTIRTKYGTNRQLQAQAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Db 61 YDYLDFGEFNOGKTIRTKYGTNRQLQAQAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Qy 121 EVNPNRNQVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQVSGEYTIETAWTRDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RDKGKWDWEVDTENGNYDYLAMVADIMDHPPEVNNELRNWGVYTTNLGLDGFRIIDAVKH 240
Db 181 RDKGKWDWEVDTENGNYDYLAMVADIMDHPPEVNNELRNWGVYTTNLGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAFKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAFKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300
Qy 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Db 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Qy 361 QGYPVFGDYGIPTGHPVPAKSKIDPILKQYAYGRNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVFGDYGIPTGHPVPAKSKIDPILKQYAYGRNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGNFVSGSVS 480
Db 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGNFVSGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485
RESULT 12
US-10-665-667-6
; Sequence 6, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjørn
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Søren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-6
Query Match 96.5%; Score 2613; DB 12; Length 485;
Best Local Similarity 95.5%; Pred. No. 7e-234;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDYLDFGEFNOGKTIRTKYGTNRQLQAQAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120

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Db 61 YDLGLGFEQKQGVTRTKYGRSLQAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTRFDPGGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Qy 181 RGDGKGDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTEDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNWHSFVDFVPLHYNLYNA 300
Db 241 IKYSFTEDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNWHSFVDFVPLHYNLYNA 300
Qy 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSVFGYDYGIPTHGVPMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKNMFAVGRNKGAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480
Db 421 HPNSGLATIMSDGAGGKNMFAVGRNKGAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485
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RESULT 13

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US-10-025-648-7
; Sequence 7, Application US/10025648
; Publication No. US20030064908A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; Svendsen, Allan
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 19-Dec-2001
; APPLICATION NUMBER: US/10/025,648
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-025-648-7
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Query Match 96.5%; Score 2613; DB 12; Length 485;

Best Local Similarity 95.5%; Pred. No. 7e-234;

Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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Qy 1 HHNCTGTMMQYFPEWYLPNDGNHNRSLRSDASNLKDGISAVWTPPAWKQASQNDVGGA 60
Db 1 HHNCTGTMMQYFPEWYLPNDGNHNRSLRSDASNLKDGISAVWTPPAWKQASQNDVGGA 60
Qy 61 YDLGLGFEQKQGVTRTKYGRSLQAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLGLGFEQKQGVTRTKYGRSLQAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTRFDPGGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Qy 181 RGDGKGDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTEDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNWHSFVDFVPLHYNLYNA 300
Db 241 IKYSFTEDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNWHSFVDFVPLHYNLYNA 300
Qy 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSVFGYDYGIPTHGVPMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKNMFAVGRNKGAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480
Db 421 HPNSGLATIMSDGAGGKNMFAVGRNKGAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485
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RESULT 14

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US-10-327-837-6
; Sequence 6, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-6

Query Match 96.5%; Score 2613; DB 12; Length 485;
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Best Local Similarity 95.5%; Pred. No. 7e-234;		Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;	
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Db	1	HHNGTGTMMQYFEWYLPNDGNHNNRLSDASNLKKGITAVWIPPAWKGASQNDVGYGA	60
QY	61	YDLYDLGEFQKGTIRTKYGTNRLOQAANALXSGIQVYGDVVMNHKGGADATEMVRV	120
Db	61	YDLYDLGEFNGKGTVRTKYGTNRLOQAATSLKNGIQVYGDVVMNHKGGADATEMVRV	120
QY	121	EVNPNRNQEVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF	180
Db	121	EVNPNRNQEVSGEYTIETAWTRDFPGRGNTHSNFKRWYHFDGVDWDSRRLNNRIYKF	180
QY	181	RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNNELRWGVWYTTTLGLDGFRIIDAVKH	240
Db	181	RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNNELRWGVWYTTTLGLDGFRIIDAVKH	240
QY	241	IKYSFTRDWINHVRSATGKNMFVAVAEFWKNDLGAENYLNKTNWNHNSVFDVPLHYNLXNA	300
Db	241	IKYSFTRDWINHVRSATGKNMFVAVAEFWKNDLGAENYLNKTNWNHNSVFDVPLHYNLXNA	300
QY	301	SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE	360
Db	301	SKSGGNYDMRNIENGTVVQRHPSHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE	360
QY	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420
Db	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420
QY	421	HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS	480
Db	421	HPNSGLATIMSDGAGGSKMFFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS	480
QY	481	IWNK 485	
Db	481	IWNK 485	
Search completed: October 7, 2004, 00:57:32			
Job time : 55.4478 secs			

QY	121	EVNPNRNQEVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF	180
Db	121	EVNPNRNQEVSGEYTIETAWTRDFPGRGNTHSNFKRWYHFDGVDWDSRRLNNRIYKF	180
QY	181	RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNNELRWGVWYTTTLGLDGFRIIDAVKH	240
Db	181	RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNNELRWGVWYTTTLGLDGFRIIDAVKH	240
QY	241	IKYSFTRDWINHVRSATGKNMFVAVAEFWKNDLGAENYLNKTNWNHNSVFDVPLHYNLXNA	300
Db	241	IKYSFTRDWINHVRSATGKNMFVAVAEFWKNDLGAENYLNKTNWNHNSVFDVPLHYNLXNA	300
QY	301	SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE	360
Db	301	SKSGGNYDMRNIENGTVVQRHPSHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE	360
QY	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420
Db	361	QGYPSVFGDYGIPTHGVPAMRSDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420
QY	421	HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS	480
Db	421	HPNSGLATIMSDGAGGSKMFFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS	480
QY	481	IWNK 485	
Db	481	IWNK 485	

Best Local Similarity 95.5%; Pred. No. 7e-234;		Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;	
QY	1	HHNGTGTMMQYFEWYLPNDGNHNNRLSDASNLKKGISAVWIPPAWKGASQNDVGYGA	60
Db	1	HHNGTGTMMQYFEWYLPNDGNHNNRLSDASNLKKGITAVWIPPAWKGASQNDVGYGA	60
QY	61	YDLYDLGEFQKGTIRTKYGTNRLOQAANALXSGIQVYGDVVMNHKGGADATEMVRV	120
Db	61	YDLYDLGEFNGKGTVRTKYGTNRLOQAATSLKNGIQVYGDVVMNHKGGADATEMVRV	120
QY	121	EVNPNRNQEVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF	180
Db	121	EVNPNRNQEVSGEYTIETAWTRDFPGRGNTHSNFKRWYHFDGVDWDSRRLNNRIYKF	180
QY	181	RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNNELRWGVWYTTTLGLDGFRIIDAVKH	240
Db	181	RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNNELRWGVWYTTTLGLDGFRIIDAVKH	240
QY	241	IKYSFTRDWINHVRSATGKNMFVAVAEFWKNDLGAENYLNKTNWNHNSVFDVPLHYNLXNA	300
Db	241	IKYSFTRDWINHVRSATGKNMFVAVAEFWKNDLGAENYLNKTNWNHNSVFDVPLHYNLXNA	300
QY	301	SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE	360
Db	301	SKSGGNYDMRNIENGTVVQRHPSHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE	360
QY	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420
Db	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420
QY	421	HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS	480
Db	421	HPNSGLATIMSDGAGGSKMFFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS	480
QY	481	IWNK 485	
Db	481	IWNK 485	
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US-10-477-725-13			
; Sequence 13, Application US/10477725			
; Publication No. US20040096952A1			
; GENERAL INFORMATION:			
; APPLICANT: NOVOZYMES A/S			
; APPLICANT: Svendsen, Allan			
; APPLICANT: Andersen, Carsten			
; APPLICANT: Thisted, Thomas			
; APPLICANT: von der Osten, Claus			
; TITLE OF INVENTION: Alpha-amylase variant with altered properties			
; FILE REFERENCE: 10182.204-US			
; CURRENT APPLICATION NUMBER: US/10/477, 725			
; CURRENT FILING DATE: 2003-11-14			
; NUMBER OF SEQ ID NOS: 13			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 13			
; LENGTH: 485			
; TYPE: PRT			
; ORGANISM: Bacillus 707			
US-10-477-725-13			
Query Match		96.5%; Score 2613; DB 16; Length 485;	
Best Local Similarity 95.5%; Pred. No. 7e-234;			
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;			
QY	1	HHNGTGTMMQYFEWYLPNDGNHNNRLSDASNLKKGISAVWIPPAWKGASQNDVGYGA	60
Db	1	HHNGTGTMMQYFEWYLPNDGNHNNRLSDASNLKKGITAVWIPPAWKGASQNDVGYGA	60
QY	61	YDLYDLGEFQKGTIRTKYGTNRLOQAANALXSGIQVYGDVVMNHKGGADATEMVRV	120
Db	61	YDLYDLGEFNGKGTVRTKYGTNRLOQAATSLKNGIQVYGDVVMNHKGGADATEMVRV	120

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-13

Perfect score: 2703

Sequence: 1 HHNGTNGTMQYPEWYLPND.....ADGKGNFVNGSGVSIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	485	2 AAW12956	AAW12956 Alpha-amy
2	2703	100.0	485	2 AAY15420	AAY15420 Termamyl-
3	2703	100.0	485	2 AAY07386	AAY07386 Wild type
4	2703	100.0	485	3 AAY99607	AAY99607 Bacillus
5	2703	100.0	485	5 ABB06939	ABB06939 Bacillus
6	2703	100.0	485	5 AAU12155	AAU12155 Bacillus
7	2703	100.0	485	5 AAB47856	AAB47856 Bacillus
8	2703	100.0	485	5 ABB76592	ABB76592 Termamyl-
9	2613	96.7	485	3 AAY97812	AAY97812 Bacillus
10	2613	96.7	485	4 AAB29260	AAB29260 Bacillus
11	2613	96.7	485	4 AAB29261	AAB29261 Bacillus
12	2613	96.7	485	5 ABB06938	ABB06938 Bacillus
13	2613	96.7	485	5 AAU12154	AAU12154 Bacillus
14	2613	96.7	485	5 AAB47855	AAB47855 Bacillus
15	2613	96.7	485	5 ABB76591	ABB76591 Termamyl-
16	2580	95.4	480	4 ABB00046	ABB00046 AA360 SEQ
17	2551	94.4	516	5 ABB08773	ABB08773 Bacillus
18	2492.5	92.2	519	4 AAE09762	AAE09762 Bacillus
19	2492.5	92.2	519	4 AAE09763	AAE09763 Bacillus
20	2484.5	91.9	519	4 AAE09767	AAE09767 Bacillus
21	2483.5	91.9	519	4 AAE09764	AAE09764 Bacillus
22	2449	90.6	485	2 AAW12110	AAW12110 Alpha-amy
23	2442	90.3	485	2 AAW12144	AAW12144 Alpha-amy
24	2442	90.3	485	2 AAW12109	AAW12109 Alpha-amy
25	2440	90.3	485	2 AAW31499	AAW31499 Bacillus

RESULT 1

AAW12956

ID AAW12956 standard; protein; 485 AA.

XX AC AAW12956;

XX DT 16-OCT-2003 (revised)

XX DT 07-APR-1997 (first entry)

XX DE Alpha-amyase.

XX KW Alpha-amyase; detergent; thermal stability; oxidation stability; enzyme;

XX KW calcium ion dependency; alpha-amyolytic activity; washing composition;

XX KW textile desizing; papermaking; beer-making; ethanol production;

XX KW sweetener.

XX OS Bacillus sp; #707.

XX PN WO9623873-A1.

XX PD 08-AUG-1996.

XX PF 05-FEB-1996; 96WO-DK000056.

XX PR 03-FEB-1995; 95DK-00000126.

XX PR 29-MAR-1995; 95DK-00000336.

XX PR 29-SEP-1995; 95DK-00001097.

XX PR 06-OCT-1995; 95DK-00001121.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Bisgard-Frantzen H, Svendsen A, Borchert T;

XX DR WPI; 1996-371423/37.

XX PT Alpha-amyase variants - with improved thermal and oxidation stability

XX PT and reduced calcium ion dependency.

XX FS Disclosure; Page 91-93; 111pp; English.

XX CC AAW12955, AAW12956, AAR81835 and AAR81836 represent the parent alpha-

XX CC amylases used to create the variants of the invention (such as AAW12098-

XX CC W12133)). This sequence represents the alpha-amyase from Bacillus sp.

XX CC #707. The variants of the invention were created using site directed, or

XX CC random, mutagenesis of the DNA sequences encoding these parent alpha-

XX CC amylases. The variants of the invention can have improved thermal

XX CC stability (such as at temperatures in the range of 40-70 degrees

XX CC Celcius), and/or oxidation stability, and/or reduced calcium ion

ALIGNMENTS

26	2440	90.3	485	2	AAW48260	Bacillus
27	2440	90.3	485	2	AAAY15421	Termamyl-
28	2440	90.3	485	2	AAAY15415	Bacillus
29	2440	90.3	485	2	AAAY25150	Bacillus
30	2440	90.3	485	2	AAAY07391	Wild type
31	2440	90.3	485	2	AAAY07381	Wild type
32	2440	90.3	485	3	AAAY99602	Bacillus
33	2440	90.3	485	3	AAAY99608	Bacillus
34	2440	90.3	485	5	ABB06933	Bacillus
35	2440	90.3	485	5	AAU12149	Bacillus
36	2440	90.3	485	5	AAB47850	Bacillus
37	2440	90.3	485	5	ABB76586	Termamyl-
38	2440	90.3	485	6	ABB99480	Amino aci
39	2438	90.2	485	2	AAW12113	Alpha-amy
40	2437	90.2	485	2	AAW12121	Alpha-amy
41	2437	90.2	485	2	AAW12099	Alpha-amy
42	2437	90.2	485	2	AAW12130	Alpha-amy
43	2437	90.2	485	2	AAW12107	Alpha-amy
44	2437	90.2	485	2	AAW12119	Alpha-amy
45	2437	90.2	485	2	AAW12102	Alpha-amy

CC dependency. The variants can also have increased alpha-amylolytic
CC activity (especially at pH values in the range of 8.5-10.5), and improved
CC binding of a particular substrate. The variant alpha-amylases also
CC possess improved specificity to a particular substrate, and/or improved
CC specificity with respect to cleavage of substrate. The variants can be
CC used in detergent and washing compositions, and for textile desizing. The
CC alpha-amylase variants can also be used in papermaking and beer-making
CC processes. The variants of the invention can also be used in the
CC production of sweeteners and ethanol from starch. (Updated on 16-OCT-2003
CC to standardise OS field)

XX Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YLDYDLGEFNGKGTVRTKYGTRSQQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YLDYDLGEFNGKGTVRTKYGTRSQQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQEVVTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
DB 121 EVNPNRNQEVVTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDWEVDTEGNYDYLMDADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
DB 181 RGHGKAWDWEVDTEGNYDYLMDADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAENYLQKTNNHNSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAENYLQKTNNHNSVDFVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485

RESULT 2

AAV15420

ID AAV15420 standard; protein; 485 AA.

XX AC AAV15420;

XX DT 22-JUL-1999 (first entry)

XX DE Termamyl-like alpha-amylase protein.

XX KW Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;

XX XW sweetener; ethanol; starch; textile desizing; starch liquefaction;

XX XW saccharification process.

XX OS Bacillus sp.

XX PN WO9923211-A1.

XX PD 14-MAY-1999.

XX 30-OCT-1998; 98WO-DK000471.
XX 30-OCT-1997; 97DK-00001240.
PR 14-JUL-1998; 98DK-00000936.
XX (NOVO) NOVO-NORDISK AS.
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
PI Kjaerulff S;
XX WPI; 1999-326987/27.
XX New Termamyl-like alpha-amylase variants.
PT Claim 38; Page 86-87; 115pp; English.
PS The specification describes termamyl-like alpha-amylase variants that
XX have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
XX Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YLDYDLGEFNGKGTVRTKYGTRSQQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YLDYDLGEFNGKGTVRTKYGTRSQQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQEVVTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
DB 121 EVNPNRNQEVVTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDWEVDTEGNYDYLMDADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
DB 181 RGHGKAWDWEVDTEGNYDYLMDADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAENYLQKTNNHNSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAENYLQKTNNHNSVDFVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485

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RESULT 3
AA07386
ID AA07386 standard; protein; 485 AA.
XX
AC AA07386;
XX
DT 16-JUL-1999 (first entry)
XX
DE Wild type Termamyl (RTM)-like alpha-amylase protein #6.
XX
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
KW ethanol.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 181..184
FT /note= "optionally 1, 2, 3 or all residues are deleted"
FT Misc-difference 195
FT /note= "optionally altered to any amino acid except an
FT Asn residue"
FT Misc-difference 206
FT /note= "optionally altered to any amino acid except an
FT Ile residue"
FT Misc-difference 212
FT /note= "optionally altered to any amino acid except a Glu
FT residue"
FT Misc-difference 216
FT /note= "optionally altered to any amino acid except a Glu
FT residue"
FT Misc-difference 269
FT /note= "optionally altered to any amino acid except a Lys
FT residue"
XX
PN W09919467-A1.
XX
XX
XX 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK000444.
XX
PR 13-OCT-1997; 97DK-00001172.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Svendsen A, Borchert TV, Bisgard-Prantzen H;
XX
DR WPI; 1999-277632/23.
XX
XX Variant alpha-amylases - useful as detergents or for textile desizing or
XX starch liquefaction.
XX
PS Claim 1; Page 70-72; 93pp; English.
XX
CC This sequence represents the parent sequence for new variants of a parent
CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants
CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
CC from either of two Bacillus species in W09526397, B. stearothermophilus,
CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
CC amylase variants are detergent additives for use in detergents for
CC dishwashing, manual or automatic laundry. The variants can also be used
CC for textile desizing or starch liquefaction (e.g. for production of
CC sweeteners or ethanol)
XX
SQ Sequence 485 AA;
XX
Query Match. 100.0%; Score 2703; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
. 1 HHNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
|||||

```

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Db 1 HHNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
QY 61 YDLYDLGEFQKGTVRTKYGTRSQLOAAVTSLNKNGIQVYGDVVNNHKGADATEMVRV 120
Db 61 YDLYDLGEFQKGTVRTKYGTRSQLOAAVTSLNKNGIQVYGDVVNNHKGADATEMVRV 120
QY 121 EVNPNRNQVETGEYTTIEAWTRFDFPCGRGNTHSFKWRWYHFDGVDWQSRRLNNRIYKF 180
Db 121 EVNPNRNQVETGEYTTIEAWTRFDFPCGRGNTHSFKWRWYHFDGVDWQSRRLNNRIYKF 180
QY 181 RHGKAWDEVDTEGNGYDLYMADIMDHPVNNELRNWGVWYNTLGLDGFRIIDAVKH 240
Db 181 RHGKAWDEVDTEGNGYDLYMADIMDHPVNNELRNWGVWYNTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHRSATGKNMFAVAREFKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHRSATGKNMFAVAREFKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGNVDMMNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTITRE 360
Db 301 SKSGNVDMMNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTITRE 360
QY 361 QGYPSVFGYGYGIPTHGVPMARSKIDPILAEARKQYAYGKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFGYGYGIPTHGVPMARSKIDPILAEARKQYAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWUNK 485
Db 481 IWUNK 485

RESULT 4
AA099607
ID AA099607 standard; protein; 485 AA.
XX
AC AA099607;
XX
DT 04-SEP-2000 (first entry)
XX
DE Bacillus Termamyl-like alpha-amylase.
XX
KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; mutein; mutant; enzyme stability; hybrid.
XX
OS Bacillus sp.
XX
PN W0200029560-A1.
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-DK000628.
XX
PR 16-NOV-1998; 98DK-00001495.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Svendsen A, Kjaerulff S, Bisgard-Prantzen H, Andersen C;
XX
DR WPI; 2000-387777/33.
XX
XX Variant of parent termamyl-like alpha amylase useful for washing, textile
XX desizing and starch liquefaction, comprising alterations in one or more
XX solvent exposed amino acid residues.
XX
PS Claim 8; Page 61-62; 80pp; English.
XX
CC The present sequence is a parent alpha-amylase from which mutants with
XX increased stability at acidic pH, low calcium concentration and high
XX temperatures have been derived. The sequence encoding this protein was

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CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of methyl
CC groups in the side chains of exposed residues may be increased. The
CC mutations can be incorporated by site-directed mutagenesis or by random
CC mutagenesis. As a result of their increased stability, the variants are
CC suitable for the industrial processing of starch, i.e. starch
CC liquefaction and saccharification. They may also be useful for washing,
CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
CC partial amino acid sequences derived from two or more alpha-amylases have
CC also been created in order to increase enzyme stability
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAMKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAMKASQNDVGYGA 60

QY 61 YDLIDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLIDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120

QY 121 EVNPNRNQEVTEGYTIEATWTRDFPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNQEVTEGYTIEATWTRDFPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180

QY 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRNWGVWYTTNLTGLDGRIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRNWGVWYTTNLTGLDGRIDAVKH 240

QY 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLQKTNNHNSVFDVPLHLYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLQKTNNHNSVFDVPLHLYNLYNA 300

QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEFKPLAYALTLTRE 360

QY 361 QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAYGKQNDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAYGKQNDYLDHNNIIGWTRGNTA 420

QY 481 IWVKN 485
DB 481 IWVKN 485

RESULT 5
ABB06939
ID ABB06939 standard; protein; 485 AA.
XX
AC ABB06939;
XX
DT 19-JUN-2002 (first entry)
XX Bacillus termamyl-like alpha-amylase protein SEQ ID NO:13.
DE
XX
KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
KW washing; sweetener; ethanol; starch.
XX
OS Bacillus sp.
XX
PN WO200166712-A2.
XX

PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-DK000144.
XX
PR 08-MAR-2000; 2000DK-00000376.
PR 15-MAR-2000; 2000US-0189857P.
PR 23-FEB-2001; 2001DK-00000303.
PR 26-FEB-2001; 2001US-0271382P.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Andersen C, Borchert TV, Nielsen BR;
XX WPI; 2002-239612/29.
DR
XX
PT Novel variant of parent termamyl-like alpha-amylase useful as a component
PT in washing and dishwashing compositions, for textile desizing, for starch
PT liquefaction, and for producing sweeteners and ethanol from starch.
XX
PS Claim 8; Page 150-151; 153pp; English.
XX
CC The present invention describes a variant of a parent termamyl-like alpha
CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
CC positions of a group of 31 possible amino acid positions. The alteration
CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
CC Gly186, Trp189, Asn195, Met202, Tyr298, Lys299, Lys302, Asn303, Asn306,
CC Arg310, Asn314, Asn320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
CC washing and/or dishwashing, textile desizing, and starch liquefaction.
CC (I) is useful as a component in hard surface cleaning detergent
CC composition, and for producing sweeteners and ethanol from starch. (I)
CC has altered solubility, preferably increased solubility, in particular
CC under washing, dish washing or hard surface cleaning conditions. The
CC present sequence represents a Bacillus termamyl-like alpha-amylase which
CC is used in the exemplification of the present invention
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAMKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAMKASQNDVGYGA 60

QY 61 YDLIDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLIDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120

QY 121 EVNPNRNQEVTEGYTIEATWTRDFPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNQEVTEGYTIEATWTRDFPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180

QY 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRNWGVWYTTNLTGLDGRIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRNWGVWYTTNLTGLDGRIDAVKH 240

QY 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLQKTNNHNSVFDVPLHLYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLQKTNNHNSVFDVPLHLYNLYNA 300

QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEFKPLAYALTLTRE 360

QY 361 QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAYGKQNDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAYGKQNDYLDHNNIIGWTRGNTA 420

QY 421 HPNSGLATIMSDGAGGSKMFFVGRNKGQVWSDITGNRTGTVTINADGWNFVSGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFFVGRNKGQVWSDITGNRTGTVTINADGWNFVSGSVS 480

QY 481 IWVWK 485
 DB 481 IWVWK 485

RESULT 6
 AAU12155
 ID AAU12155 standard; protein; 485 AA.
 AC AAU12155;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Bacillus TERMAMYL-like alpha-amylase 707.
 XX
 KW TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
 KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KW amylopectin; limit dextrin; NOVAMYL; 707.
 XX
 OS Bacillus sp.
 XX
 PN WO2001188107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI; 2002-106123/14.
 XX
 PT New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 5; Page 81-83; 84pp; English.
 CC The invention relates to a variant of parent TERMAMYL-like alpha- amylase
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyl-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha- amylase, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning
 CC detergent composition, and for producing sweeteners from starch. The
 CC variant has altered alpha-1,6-D-glucosidic branch linkage cleavage
 CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
 CC branch linkage cleavage activity of amylopectin or a limit dextrin
 CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
 CC natural variant of the TERMAMYL alpha-amylase, 707
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 5.3e-219;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTWQYFEWYLPNDGNHWRNLNSDASNLKSGITAVWTPPAWKASQNDVCYGA 60
 DB 1 HNGTGTWQYFEWYLPNDGNHWRNLNSDASNLKSGITAVWTPPAWKASQNDVCYGA 60
 QY 61 YLDYDLGEFNGKQVTRTKYGRSLOQAQVTSKXNGIQVYGVGVVNMHKGADATEMVRV 120
 DB 61 YLDYDLGEFNGKQVTRTKYGRSLOQAQVTSKXNGIQVYGVGVVNMHKGADATEMVRV 120

121 EVNPNRNRQEVTCGYTTEAWTRDFPGRGNTHSSFKRWYHFDGVDWDSRLNNRIYKF 180
 121 EVNPNRNRQEVTCGYTTEAWTRDFPGRGNTHSSFKRWYHFDGVDWDSRLNNRIYKF 180
 181 RGHGKAWDEVDYENGNYDYLMTADI DMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
 181 RGHGKAWDEVDYENGNYDYLMTADI DMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
 241 IKYSFTRDWINHVRSAATGKMFVABFVKNDLGAIEENYLOKTNWNHVSFVDFPLHYNLYNA 300
 241 IKYSFTRDWINHVRSAATGKMFVABFVKNDLGAIEENYLOKTNWNHVSFVDFPLHYNLYNA 300
 301 SKSGNDYDMENIFNGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEFKPLAYALTITRE 360
 301 SKSGNDYDMENIFNGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEFKPLAYALTITRE 360
 361 QGVPSEVFGYDYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
 361 QGVPSEVFGYDYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTGTINADGWNFSVNGSGVS 480
 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTGTINADGWNFSVNGSGVS 480
 481 IWVWK 485
 481 IWVWK 485

RESULT 7
 AAB47856
 ID AAB47856 standard; protein; 485 AA.
 AC AAB47856;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Bacillus alpha amylase 707.
 XX
 KW Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KW cured meat; fermented meat; spice.
 XX
 OS Bacillus sp.
 XX
 PN WO2001196537-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-DK000404.
 XX
 PR 14-JUN-2000; 2000DK-00000917.
 PR 20-JUN-2000; 2000US-0212852P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Nielsen BR, Weibye M;
 XX
 DR WPI; 2002-098064/13.
 XX
 PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 5; Page 44-46; 47pp; English.
 CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl- like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30

CC kda has been provided. The product comprises a maltodextrin with a DE of
CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The
CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
CC where the glucose syrup is useful as an ingredient in food, feed or
CC pharmaceuticals. Glucose syrup is useful in confectionery such as
CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
CC dairy and ice cream such as coffee whiteners, conventional foods such as
CC salad dressings, and food ingredients and preparations such as cured
CC meat, fermented meat, spices and seasoning encapsulated flavours
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGFEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQYVGVVNMHKGADATEMVRV 120
DB 61 YDLYDLGFEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQYVGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
DB 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNNGVYNTLGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNNGVYNTLGLDGFRI DAVKH 240
QY 241 IKYSFTTRDWINHVRSGATGKNMFAVAFWKNDLGA IENYLQKTNNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTTRDWINHVRSGATGKNMFAVAFWKNDLGA IENYLQKTNNHNSVFDVPLHYNLYNA 300
QY 301 SKSGGNYDMRNI FNGTVVQRHPSHATVFDNHD SQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNI FNGTVVQRHPSHATVFDNHD SQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDP ILEARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDP ILEARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATTMSDAGGSKWFMVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATTMSDAGGSKWFMVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 8
ABB76592
ID ABB76592 standard; protein; 485 AA.
XX
AC ABB76592;
XX
19-AUG-2002 (first entry)
XX
Termamyl¹-like-alpha-amylase #7.
XX
Termamyl¹; alpha amylase; starch liquefaction; ethanol production;
KW textile desizing; detergent; enzyme.
XX
Bacillus sp.
XX
WO200210355-A2.
XX
07-FEB-2002.
XX
12-JUL-2001; 2001WO-DK000488.

XX
PR 01-AUG-2000; 2000DK-00001160.
PR 12-SEP-2000; 2000DK-00001354.
PR 10-NOV-2000; 2000DK-00001687.
PR 26-APR-2001; 2001DK-00000655.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Thisted T, Kjaerulff S, Andersen C, Fugleang CC;
XX
DR WPI; 2002-280633/32.
XX
PT Variant of parent Termamyl¹-like alpha amylase, useful in detergent
PT compositions, for starch liquefaction, ethanol production, washing and/or
PT dish washing, and textile desizing.
XX
PS Claim 8; Page 76-78; 90pp; English.
XX
CC This invention relates to variants of a parent Termamyl¹-like alpha-
CC amylases. These are used for starch liquefaction, ethanol production,
CC detergent, and textile desizing. The amylases have altered stability,
CC particularly at high temperatures from 70-120plusoC and low pH in the
CC range from pH 4.0-6.0. The present sequence is a termamyl¹-like-alpha-
CC amylase
XX
SQ Sequence 485 AA;
Query Match 100.0%; Score 2703; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGFEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQYVGVVNMHKGADATEMVRV 120
DB 61 YDLYDLGFEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQYVGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
DB 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNNGVYNTLGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNNGVYNTLGLDGFRI DAVKH 240
QY 241 IKYSFTTRDWINHVRSGATGKNMFAVAFWKNDLGA IENYLQKTNNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTTRDWINHVRSGATGKNMFAVAFWKNDLGA IENYLQKTNNHNSVFDVPLHYNLYNA 300
QY 301 SKSGGNYDMRNI FNGTVVQRHPSHATVFDNHD SQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNI FNGTVVQRHPSHATVFDNHD SQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDP ILEARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDP ILEARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATTMSDAGGSKWFMVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATTMSDAGGSKWFMVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485
RESULT 9
AAY97812
ID AAY97812 standard; protein; 485 AA.
XX
AC AAY97812;

XX 12-SEP-2003 (revised)
 DT 21-AUG-2000 (first entry)
 DE Bacillus alkaline alpha-amylase AA560.
 XX Alkaline alpha-amylase; AA560; immunogenicity; allergenicity;
 KW industrial product; pharmaceutical; hypoallergenic.
 XX Bacillus sp; 'DSM12649'.
 XX W0200022103-A1.
 XX 20-APR-2000.
 XX 12-OCT-1999; 99WO-DK000542.
 XX 13-OCT-1998; 98DK-00001301.
 PR 04-OCT-1999; 99DK-00001418.
 XX (NOVO) NOVO-NORDISK AS.
 XX Olsen AA, Von Der Osten C, Andersen KV, Ernst S, Roggen EL;
 DR WPI; 2000-329163/28.
 DR N-PSDB; AAA30783.
 XX New modified polypeptides having an attached polymer for reducing immune
 PT responses, useful in e.g. detergents, cleaning products, skin care
 PT products, food or feed products, textile products or pharmaceuticals.
 XX Example 4; Page 102-105; 108pp; English.
 XX The invention relates to proteins with reduced immunogenicity, having one
 CC or more modified amino acids, where the alpha-carbon atoms of the amino
 CC acids are located less than 15 Angstroms from a ligand bound to the
 CC protein. The modification may entail substitution of the endogenous
 CC residue for a non-endogenous residue and/or attachment of polymeric
 CC molecules such as carbohydrates or branched polyethylene glycols to the
 CC amino acid residues. The residue to be modified is identified from the 3-
 CC dimensional structure of the protein determined, for example, by X-ray
 CC crystallography or NMR. A wide variety of enzymes may be modified
 CC according to the invention, including proteases (especially subtilisins),
 CC carbohydrases (such as amylase), isomerases, transferases and
 CC oxidoreductases. The modified proteins of the invention may be used for
 CC reducing the allergenicity of industrial products (i.e., those which are
 CC not intended to enter the circulatory system. The proteins which are
 CC cleaning agents (such as laundry products, dish-washing products or hard
 CC surface cleaning products), skin-care products, textile treatment
 CC products (e.g., bleaching agents) and food products. The modified
 CC polypeptides can also be used for reducing the immunogenicity of
 CC pharmaceuticals. The modified proteins have reduced immunogenicity or
 CC allergenicity while maintaining a high percentage of activity. The
 CC present sequence represents an alkaline alpha-amylase, AA560, from
 CC Bacillus DSM 12649, which may be modified according to the invention.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 XX Sequence 485 AA;
 SQ
 Query Match 96.7%; Score 2613; DB 3; Length 485;
 Best Local Similarity 95.5%; Pred. No. 2e-211;
 Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 HNGTNGTMMQYFEWYLPDNGNHNRLNSDASNLKSGITAVTIPPAWKASQNDVGYGA 60
 DB 1 HNGTNGTMMQYFEWYLPDNGNHNRLNSDASNLKSGISAVTIPPAWKASQNDVGYGA 60
 QY 61 YDLYDLGEFNQKGVTRTKYGRSOLQAATVSLKNGGIQVYGDVVMNKHGGADATEMVRV 120
 DB 61 YDLYDLGEFNQKGVTRTKYGRNQLQAANVALKSNGIQVYGDVVMNKHGGADATEMVRV 120
 QY 121 EVNPNRNEQVSGEYTTIEAWTKFDPGRGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
 DB 121 EVNPNRNEQVSGEYTTIEAWTKFDPGRGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
 QY 181 RGCHKAWDEVDVTENGNDYLMYADIDMDHPEVNVNLRNMGVWYNTTGLDGFRIIDAVKH 240
 DB 181 RGCHKAWDEVDVTENGNDYLMYADIDMDHPEVNVNLRNMGVWYNTTGLDGFRIIDAVKH 240
 QY 241 IKYSFTRDWINHVSATGKNMFAVAEFKNDLGAIEYLOKTNWNHVSFVDFPLHYNLYNA 300
 DB 241 IKYSFTRDWINHVSATGKNMFAVAEFKNDLGAIEYLOKTNWNHVSFVDFPLHYNLYNA 300
 QY 301 SKSGNTDMRNI FNGTVVQRHPSHAFTVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
 DB 301 SKSGNTDMRNI FNGTVVQRHPSHAFTVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
 QY 361 QGYSVFVGDYVGIPTHGVPAMRSKIDPILKAROKYAGKONDYLDHNIIGWTREGNTA 420
 DB 361 QGYSVFVGDYVGIPTHGVPAMRSKIDPILKAROKYAGKONDYLDHNIIGWTREGNTA 420
 QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKGAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
 DB 421 HPNSGLATIMSDGAGGSKMFMVGRNKGAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
 QY 481 IWVKN 485
 DB 481 IWVKN 485
 RESULT 10
 AAB29260
 ID AAB29260 standard; protein; 485 AA.
 XX AC AAB29260;
 XX DT 07-FEB-2001 (first entry)
 XX DE Bacillus sp. alpha-amylase #1.
 XX KW Alpha-amylase; laundry; detergent; textile desizing;
 KW sweetener production; ethanol production; brewing; paper production.
 OS Bacillus sp.
 PN W0200060060-A2.
 XX 12-OCT-2000.
 XX 28-MAR-2000; 2000WO-DK000149.
 XX 31-MAR-1999; 99DK-00000439.
 PR 13-APR-1999; 99DK-00000490.
 PR 13-APR-1999; 99US-00290734.
 XX (NOVO) NOVO NORDISK AS.
 XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
 FI Blegard-Frantzen H, Svendsen A, Andersen C;
 XX WPI; 2001-006814/01.
 DR N-PSDB; AAC63114.
 XX New polypeptides having alpha-amylase activity and nucleic acids encoding
 PT the enzymes, useful as a detergent or a dishwash detergent composition,
 PT for textile desizing, for liquefaction of starch, or for ethanol
 PT production.
 XX Claim-3; Page 106-108; 116pp; English.
 XX The present invention relates to proteins having alpha-amylase activity
 CC and their coding sequences. These proteins are useful in a number of
 CC industrial applications, including detergents, hard surface cleaning
 CC compositions, in compositions for desizing textiles, fabrics and
 CC garments, in the production of pulp and paper, in beer-making and
 CC brewing, and in starch conversion processes such as sweetener and ethanol

```
CC production
XX SQ Sequence 485 AA;

Query Match
Best Local Similarity 96.7%; Score 2613; DB 4; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGISAVWIPPAWKASQNDVGYGA 60

QY 61 YDLVDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVNMHKGADATEMVRV 120
DB 61 YDLVDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVNMHKGADATEMVRV 120

QY 121 EVNPNRNQEVGTGEYTIETAWTRDFPGRGNTHSFKRWYHFDGVWDQSRRLNNRIYKF 180
DB 121 EVNPNRNQEVGTGEYTIETAWTRDFPGRGNTHSFKRWYHFDGVWDQSRRLNNRIYKF 180

QY 181 RHGKAWDEVDTEGNYDYLMTADIMDHPVNNELRNWGVWYTNLTGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNYDYLMTADIMDHPVNNELRNWGVWYTNLTGLDGFRIIDAVKH 240

QY 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNKDLGAIENYLOKTNWHSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNKDLGAIENYLOKTNWHSVDFVPLHYNLYNA 300

QY 301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDQSPEEALSFVEEWFKEPLAYALTITRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDQSPEEALSFVEEWFKEPLAYALTITRE 360

QY 361 QGYPSFYGDYIGIPTHGVPAKSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSFYGDYIGIPTHGVPAKSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 480

QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 11
AAB29261
ID AAB29261 standard; protein; 485 AA.
XX
AC AAB29261;
XX
XX
DT 07-FEB-2001 (first entry)
XX
DE Bacillus sp. alpha-amylase #2.
XX
KW Alpha-amylase; laundry; detergent; textile desizing;
KW sweetener production; ethanol production; brewing; paper production.
XX
XX Bacillus sp.
XX
XX W0200060060-A2.
XX
XX 12-OCT-2000.
XX
XX 28-MAR-2000; 2000WO-DX000149.
XX
XX 31-MAR-1999; 99DK-00000439.
XX
XX 13-APR-1999; 99DK-00000490.
XX
XX 13-APR-1999; 99US-00290734.
XX
XX (NOVO ) NOVO NORDISK AS.
XX
XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
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PI Bisgard-Frantzen H, Svendsen A, Andersen C;
XX WPI: 2001-006814/01.
DR N-PSDB; AAC63115.
XX
PT New polypeptides having alpha-amylase activity and nucleic acids encoding
PT the enzymes, useful as a detergent or a dishwash detergent composition,
PT for textile desizing, for liquefaction of starch, or for ethanol
PT production.
XX
XX Claim 3; Page 111-112; 116pp; English.
XX
XX The present invention relates to proteins having alpha-amylase activity
CC and their coding sequences. These proteins are useful in a number of
CC industrial applications, including detergents, hard surface cleaning
CC compositions, in compositions for desizing textiles, fabrics and
CC garments, in the production of pulp and paper, in beer-making and
CC brewing, and in starch conversion processes such as sweetener and ethanol
CC production.
XX
XX Sequence 485 AA;
SQ
Query Match
Best Local Similarity 96.7%; Score 2613; DB 4; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGISAVWIPPAWKASQNDVGYGA 60

QY 61 YDLVDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVNMHKGADATEMVRV 120
DB 61 YDLVDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVNMHKGADATEMVRV 120

QY 121 EVNPNRNQEVGTGEYTIETAWTRDFPGRGNTHSFKRWYHFDGVWDQSRRLNNRIYKF 180
DB 121 EVNPNRNQEVGTGEYTIETAWTRDFPGRGNTHSFKRWYHFDGVWDQSRRLNNRIYKF 180

QY 181 RHGKAWDEVDTEGNYDYLMTADIMDHPVNNELRNWGVWYTNLTGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNYDYLMTADIMDHPVNNELRNWGVWYTNLTGLDGFRIIDAVKH 240

QY 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNKDLGAIENYLOKTNWHSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVEFKNKDLGAIENYLOKTNWHSVDFVPLHYNLYNA 300

QY 301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDQSPEEALSFVEEWFKEPLAYALTITRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDQSPEEALSFVEEWFKEPLAYALTITRE 360

QY 361 QGYPSFYGDYIGIPTHGVPAKSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSFYGDYIGIPTHGVPAKSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 480

QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 12
AAB06938
ID AAB06938 standard; protein; 485 AA.
XX
XX
AC AAB06938;
XX
XX 19-JUN-2002 (first entry)
XX
XX Bacillus termamyl-like alpha-amylase protein SEQ ID NO:12.
XX
```

Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
washing; sweetener; ethanol; starch.
Bacillus sp.
W0200166712-A2.
13-SEP-2001.
07-MAR-2001; 2001WO-DK000144.
08-MAR-2000; 2000DK-00000376.
15-MAR-2000; 2000US-0189857P.
23-FEB-2001; 2001DK-00000303.
26-FEB-2001; 2001US-0271382P.
(NOVO) NOVOZYMES AS.
Andersen C, Borchert TV, Nielsen BR;
WPI; 2002-239612/29.
N-PSDB; ABL50569.
Novel variant of parent termamyl-like alpha-amylase useful as a component
in washing and dishwashing compositions, for textile desizing, for starch
liquefaction, and for producing sweeteners and ethanol from starch.
Claim 1; Page 148-149; 153pp; English.
The present invention describes a variant of a parent termamyl-like alpha
-amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
positions of a group of 31 possible amino acid positions. The alteration
in (I) may be at Arg28, Arg118, Asn174, Asn181, Gly182, Asp183, Gly184,
Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
washing and/or dishwashing, textile desizing, and starch liquefaction.
(I) is useful as a component in hard surface cleaning detergent
composition, and for producing sweeteners and ethanol from starch. (I)
has altered solubility, preferably increased solubility, in particular
under washing, dish washing or hard surface cleaning conditions. The
present sequence represents a Bacillus termamyl-like alpha-amylase which
is used in the exemplification of the present invention
Sequence 485 AA;
Query Match 96.7%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 2e-211;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRNLSNASLKSXGITAIVIPPAWKQASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRNLSNASLKSXGITAIVIPPAWKQASQNDVGYGA 60
QY 61 YDLVLDGEFQKGVTRKYGRSLOARVTSLNKNGIQVYGVGVVNHKGGADATEMVRV 120
DB 61 YDLVLDGEFQKGVTRKYGRSLOARVTSLNKNGIQVYGVGVVNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGYTTEAWTRFPDGRGNTHSSFKWRVYHFDGVDWQSRRLNRYKF 180
DB 121 EVNPNRNRQEVGTGYTTEAWTRFPDGRGNTHSSFKWRVYHFDGVDWQSRRLNRYKF 180
QY 181 RGHGKAWDEVDTEGNYDYLMYADI DMHDPEVVNRLNNGVWYTTTLGLDGFIDAVKH 240
DB 181 RGDGKGWDEVDTEGNYDYLMYADI DMHDPEVVNRLNNGVWYTTTLGLDGFIDAVKH 240
QY 241 IKYSFTRDWLNHVSATGKNMFAVEFWKNDLGAIEYLNQTNHNSVDFVPLHNLNYA 300
DB 241 IKYSFTRDWLNHVSATGKNMFAVEFWKNDLGAIEYLNQTNHNSVDFVPLHNLNYA 300
QY 301 SKSGNVDNRINFGTVVQRHPHSHAVTFVDNHDSPQEALESFVEWFKPLAYALTLTRE 360
DB 301 SKSGNVDNRINFGTVVQRHPHSHAVTFVDNHDSPQEALESFVEWFKPLAYALTLTRE 360

Db 301 SKSGNVDNRINFGTVVQRHPHSHAVTFVDNHDSPQEALESFVEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTTGVPAMRSKIDPILFAROKYAYGKONDYLDHNIIGWTREGNTA 420
Db 361 QGYPSVFYGDYGIPTTGVPAMRSKIDPILFAROKYAYGKONDYLDHNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWNK 485
Db 481 IWNK 485
RESULT 13
AAU12154
ID AAU12154 standard; protein; 485 AA.
XX AC AAU12154;
XX AC AAU12154;
DT 09-APR-2002 (first entry)
XX Bacillus TERMAMYL-like alpha-amylase AA560.
DE TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
KW amylopectin; limit dextrin; NOVAMYL; AA560.
XX Bacillus sp.
OS W0200188107-A2.
XX W0200188107-A2.
XX 22-NOV-2001.
XX 10-MAY-2001; 2001WO-DK000323.
XX 12-MAY-2000; 2000DK-00000779.
XX (NOVO) NOVOZYMES AS.
XX Svendsen A, Jorgensen CT, Nielsen BR;
XX WPI; 2002-106123/14.
XX N-PSDB; AAS20027.
XX New variant of parent Termamyl-like alpha-amylase for use as a component
in washing and dishwashing compositions, for textile desizing, for starch
liquefaction, and for producing sweeteners and ethanol from starch.
XX Claim 5; Page 78-81; 84pp; English.
XX The invention relates to a variant of parent TERMAMYL-like alpha- amylase
comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
or at position 234, where the variant has alpha-amylase activity and each
position corresponds to a position of a parent Termamyl-like alpha-
amylase sequence having a Bacillus licheniformis alpha-amylase sequence
of 483 amino acids, given in specification. The variant alpha- amylase, a
detergent additive comprising the variant or a detergent composition
comprising the variant, is useful for washing and/or dishwashing or
textile desizing. The alpha-amylase is useful for starch liquefaction or
ethanol production and as a component in a hard surface cleaning
detergent composition, and for producing sweeteners from starch. The
variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
branch linkage cleavage activity of amylopectin or a limit dextrin
prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
natural variant of the TERMAMYL alpha-amylase, AA560
Sequence 485 AA;
Query Match 96.7%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 2e-211;

		Matches	463;	Conservative	13;	Mismatches	9;	Indels	0;	Gaps	0;
QY	1	HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKASQNDVGYGA	60								
Db	1	HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGISAVWIPPAWKASQNDVGYGA	60								
QY	61	YDYLDFGNQKGTIRTKYGRSOLQAATVSLKNGIOVYGDVVMHKGADATEMVRV	120								
Db	61	YDYLDFGNQKGTIRTKYGRSOLQAATVSLKNGIOVYGDVVMHKGADATEMVRV	120								
QY	121	EVNPNRNRQSVTGEYTIETAWTRDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKF	180								
Db	121	EVNPNRNRQSVTGEYTIETAWTRDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKF	180								
QY	181	RHGKAWDEVDTEENGNDYLMYADIDMDHPEVNNELRNWGVYTTNTLGLDGFPRIDAVKH	240								
Db	181	RGDGKGDWEVDTEENGNDYLMYADIDMDHPEVNNELRNWGVYTTNTLGLDGFPRIDAVKH	240								
QY	241	IKYSFTRDWINHVRSATGKMFAVEFWKNDLGAENLYLQKTWNHSHVFDVPLHYNLNA	300								
Db	241	IKYSFTRDWINHVRSATGKMFAVEFWKNDLGAENLYLQKTWNHSHVFDVPLHYNLNA	300								
QY	361	QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAGQNDYLDHNNIIGWTREGNTA	420								
Db	361	QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAGQNDYLDHNNIIGWTREGNTA	420								
QY	421	HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS	480								
Db	421	HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS	480								
QY	481	IWYNK 485									
Db	481	IWYNK 485									
RESULT 15											
AB76591	ID	ABB76591	standard; protein; 485 AA.								
XX	AC	ABB76591;									
XX	AC	ABB76591;									
DT	DT	19-AUG-2002	(first entry)								
XX	XX	Termamyl-like-alpha-amylase #6.									
RESULT 14											
AB76591	ID	AB76591	standard; protein; 485 AA.								
XX	AC	AB76591;									
XX	AC	AB76591;									
DT	DT	02-APR-2002	(first entry)								
XX	XX	Bacillus alpha amylase AA560.									
DE	DE	Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;									
KW	KW	starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;									
KW	KW	bakery; cereal bar; ice cream; coffee whitener; salad dressing;									
KW	KW	cured meat; fermented meat; spice.									
XX	XX	Bacillus sp.									
OS	OS	WO2001.96537-A2.									
PN	PN	20-DEC-2001.									
XX	XX	13-JUN-2001; 2001WO-DK000404.									
XX	XX	14-JUN-2000; 2000DK-00000917.									
PR	PR	20-JUN-2000; 2000US-0212852P.									
XX	XX	(NOVO) NOVOZYMES AS.									
PA	PA	Nielsen BR, Weibye M;									
XX	XX	WPI; 2002-098064/13.									
DR	DR	N-PSDB; AA172216.									
XX	XX	New modified alpha-amylase derived from the genus Bacillus and/or is a									
PT	PT										

PT	Termamyl-like alpha-amylase, which has been pre-oxidized for producing maltodextrin or glucose syrup.
PT	Claim 5; Page 43-44; 47pp; English.
XX	The sequences given in AAB47850-56 show modified alpha-amylases derived from the genus Bacillus. These alpha amylases are Termamyl-like alpha-amylase and they have been pre-oxidized. The alpha amylase is useful for producing a maltodextrin or glucose syrup, by treating starch with a pre-oxidized alpha-amylase until a product with a DE between 5-45 has been provided and/or until a product with a molecular weight of between 5-30 kda has been provided. The product comprises a maltodextrin with a DE of 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The alpha amylase is useful for producing a maltodextrin or glucose syrup, where the glucose syrup is useful as an ingredient in food, feed or pharmaceuticals. Glucose syrup is useful in confectionery such as candies, beverages such as isotonic drinks, bakery such as cereal bars, dairy and ice cream such as coffee whiteners, conventional foods such as salad dressings, and food ingredients and preparations such as cured meat, fermented meat, spices and seasoning encapsulated flavours
XX	Sequence 485 AA;
QY	Query Match 96.7%; Score 2613; DB 5; Length 485;
Db	Best Local Similarity 95.5%; Pred. No. 2e-211; Mismatches 13; Indels 0; Gaps 0;
QY	1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
Db	1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGISAVWIPPAWKASQNDVGYGA 60
QY	61 YDYLDFGNQKGTIRTKYGRSOLQAATVSLKNGIOVYGDVVMHKGADATEMVRV 120
Db	61 YDYLDFGNQKGTIRTKYGRSOLQAATVSLKNGIOVYGDVVMHKGADATEMVRV 120
QY	121 EVNPNRNRQSVTGEYTIETAWTRDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKF 180
Db	121 EVNPNRNRQSVTGEYTIETAWTRDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKF 180
QY	181 RHGKAWDEVDTEENGNDYLMYADIDMDHPEVNNELRNWGVYTTNTLGLDGFPRIDAVKH 240
Db	181 RGDGKGDWEVDTEENGNDYLMYADIDMDHPEVNNELRNWGVYTTNTLGLDGFPRIDAVKH 240
QY	241 IKYSFTRDWINHVRSATGKMFAVEFWKNDLGAENLYLQKTWNHSHVFDVPLHYNLNA 300
Db	241 IKYSFTRDWINHVRSATGKMFAVEFWKNDLGAENLYLQKTWNHSHVFDVPLHYNLNA 300
QY	301 SKSGGNDYMRNIFNGTVVQRPVSHAVTFVDNHDQSRRLNNRIYKF 360
Db	301 SKSGGNDYMRNIFNGTVVQRPVSHAVTFVDNHDQSRRLNNRIYKF 360
QY	361 QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAGQNDYLDHNNIIGWTREGNTA 420
Db	361 QGYPSVFGDYGIPTHGVPAMRSKIDPILAEARQKYAGQNDYLDHNNIIGWTREGNTA 420
QY	421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db	421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY	481 IWYNK 485
Db	481 IWYNK 485
RESULT 15	
AB76591	ID ABB76591 standard; protein; 485 AA.
XX	AC ABB76591;
XX	AC ABB76591;
DT	DT 19-AUG-2002 (first entry)
XX	XX Termamyl-like-alpha-amylase #6.

XX Termamyl; alpha amylase; starch liquefaction; ethanol production;
KW textile desizing; detergent; enzyme.
XX
OS Bacillus sp.
XX
PN WO200210355-A2.
XX
PD 07-FEB-2002.
XX
PF 12-JUL-2001; 2001WO-DK000488.
XX
PR 01-AUG-2000; 2000DK-00001160.
PR 12-SEP-2000; 2000DK-00001354.
PR 10-NOV-2000; 2000DK-00001687.
PR 26-APR-2001; 2001DK-00000655.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Thisted T, Kjaerulff S, Andersen C, Fugleang CC;
XX
DR WPI; 2002-280633/32.
DR N-PSDB; ABL96212.
XX
PT Variant of parent Termamyl-like alpha amylase, useful in detergent
PT compositions, for starch liquefaction, ethanol production, washing and/or
PT dish washing, and textile desizing.
XX
PS Claim 8; Page 75-76; 90pp; English.
XX
CC This invention relates to variants of a parent Termamyl-like alpha-
CC amylases. These are used for starch liquefaction, ethanol production,
CC detergent, and textile desizing. The amylases have altered stability,
CC particularly at high temperatures from 70-120plusOC and low pH in the
CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
CC amylase
XX
SQ Sequence 485 AA;

Query Match 96.7%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 2e-211;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
DB 1 HHNGTNGTMQYFEWYLPNDGNHNRNLRSASNLKSGISAVWIPPAWKASQNDVGGA 60
QY 61 YDLYDLGEFQKGTVRTKYGTRSQLOAAVTSKXNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFQKGTVRTKYGTRNQLOAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVGTTEATWTRPDPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNRQEVSGEYTTAEATKFPDPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGHGKAWDEVDTENGNDYLYMADI DMHDPVVNLELNMGVWYTTNLGLDGFRI DAVKH 240
DB 181 RGDGKGWDEVDTENGNDYLYMADI DMHDPVVNLELNMGVWYTTNLGLDGFRI DAVKH 240
QY 241 IKYSFTRDWINHRSATGKMFVAEFAEKNDLGAENYLOKTNWNSHVFDPVPLHNLNA 300
DB 241 IKYSFTRDWINHRSATGKMFVAEFAEKNDLGAENYLNKTNWNSHVFDPVPLHNLNA 300
QY 301 SKSGGNDYDMEINFGTVVQRHSHAVTFVNDHDSQPEALESFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNDYDMEQIFNGTVVQRHSHAVTFVNDHDSQPEALESFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
|||||

Db 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVVK 485
|||
Db 481 IWVVK 485

Search completed: October 7, 2004, 00:12:25
Job time : 59.5516 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-13

Perfect score: 2703

Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGWNFSVNGSGSVIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	518	1 A27705	alpha-amylase (EC
2	1876	69.4	512	1 ALBSL	alpha-amylase (EC
3	1874.5	69.3	549	1 A54541	alpha-amylase (EC
4	1867.5	69.1	549	1 A24549	alpha-amylase (EC
5	1866.5	69.1	549	1 A24436	alpha-amylase (EC
6	1836	67.9	514	1 ALBSN	alpha-amylase (EC
7	1817	67.2	548	1 ALBSF	alpha-amylase (EC
8	1360	50.3	493	2 S15713	alpha-amylase (EC
9	1280	47.4	484	2 G95160	alpha-amylase (imp
10	1278	47.3	484	2 P98026	alpha-amylase (EC
11	1275	47.2	492	2 AH2079	alpha-amylase (imp
12	1139	42.1	491	2 C86781	alpha-amylase (imp
13	1125	41.6	506	2 G98247	cytoplasmic alpha-
14	1124	41.6	495	2 AD3038	alpha-amylase (imp
15	1074	39.7	494	1 B45738	alpha-amylase (EC
16	1064	39.4	494	2 AD0751	cytoplasmic alpha-
17	1054	39.0	495	2 B90922	cytoplasmic alpha-
18	1045	38.7	495	1 A45738	alpha-amylase (EC
19	1035	38.3	495	2 B95810	cytoplasmic alpha-
20	362.5	13.4	217	2 A19506	alpha-amylase (EC
21	331	12.2	1196	2 A29130	beta-amylase (EC 3
22	311.5	11.5	482	2 S31478	alpha-amylase (EC
23	285	10.5	504	2 A55861	alpha-amylase (EC
24	281.5	10.4	421	2 S10514	alpha-amylase (EC
25	277	10.2	423	2 T09942	alpha-amylase (EC
26	276	10.2	440	2 S14958	alpha-amylase (EC
27	266.5	9.9	435	2 JC7137	alpha-amylase (EC
28	266	9.8	826	2 E96720	probable alpha-amy
29	265	9.8	437	2 S14956	alpha-amylase (EC

RESULT 1

A27705

alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase

C;Species: Bacillus sp.

C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

C;Accession: A27705

R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.

Biochem. Biophys. Res. Commun. 151, 25-31, 1988

A;Title: Nucleotide sequence of the maltotetraose-producing amylase gene from an alkalophilic

A;Reference number: A27705; MUID:88162814; PMID:3258152

A;Accession: A27705

A;Molecule type: DNA

A;Residues: 1-518 <TSU>

A;Cross-references: GB:M18862; NID:G142496; PIDN:AAA22231.1; PID:G142497

A;Experimental source: chromosomal DNA of strain 707

A;Note: amino end of mature protein also determined

C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F;1-33/Domain: signal sequence #status predicted <SIG>

F;34-518/Product: alpha-amylase #status experimental <MAT>

F;236-369/Domain: alpha-amylase core homology <AMY>

F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted

F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2703; DB 1; Length 518;

Best Local Similarity 100.0%; Pred. No. 8.9e-179;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASLKSIGITAVWIPPAWKASQNDVGYGA 60

Db 34 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASLKSIGITAVWIPPAWKASQNDVGYGA 93

Qy 61 YDLYDLGEFQKGTVRTKYGTRSQQAQAVTSLKNGGIQVYGDVVMNHKGGADATEMVRV 120

Db 94 YDLYDLGEFQKGTVRTKYGTRSQQAQAVTSLKNGGIQVYGDVVMNHKGGADATEMVRV 153

Qy 121 EVNPNNRNQVTEGYTTEAWTRFDPGNGNTHSFKWRVHFGVDVMDQSRRLNNRIYKF 180

Db 154 EVNPNNRNQVTEGYTTEAWTRFDPGNGNTHSFKWRVHFGVDVMDQSRRLNNRIYKF 213

Qy 181 RGHGKAWDEVDTEGNYDLYMADIDMDHPEVNNELRNHGVWYNTLTGLDGEFRIDAVKH 240

Db 214 RGHGKAWDEVDTEGNYDLYMADIDMDHPEVNNELRNHGVWYNTLTGLDGEFRIDAVKH 273

Qy 241 IKYSFTRDWLNHVRSAATGKNMFAVAEFWKNKDLGAIENYLOKTNWNHVSFVDFVPLHNLNA 300

Db 274 IKYSFTRDWLNHVRSAATGKNMFAVAEFWKNKDLGAIENYLOKTNWNHVSFVDFVPLHNLNA 333

ALIGNMENTS

QY 301 SKSGNVDNRNIENGTVVQHPHSHAVTFVDNHDSDQPEALLESFVEEWPFKPLAYALTITRE 360
Db |||||
QY 334 SKSGNVDNRNIFNGTVVQHPHSHAVTFVDNHDSDQPEALLESFVEEWPFKPLAYALTITRE 393
Db |||||
QY 361 QGYPSVFYGDYIGPTHGVPAMRSKIDPILFARQKAYGKQNDYLDHNIIGWTRGNTA 420
Db |||||
QY 394 QGYPSVFYGDYIGPTHGVPAMRSKIDPILFARQKAYGKQNDYLDHNIIGWTRGNTA 453
QY 421 HPNSGLATINSDGAGGSKMFWGVRNKGAGQVMSDITGNRTGTGTINADGWGNFVNGGSVS 480
Db |||||
QY 454 HPNSGLATINSDGAGGSKMFWGVRNKGAGQVMSDITGNRTGTGTINADGWGNFVNGGSVS 513
QY 481 IWNK 485
Db |||||
QY 514 IWNK 518
Db |||||
RESULT 2
ALBSL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus licheniformis
C;Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
C;Accession: A91997; B24549; A21663; I39774; I39772; A26151; S53788; A00844
R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uchida, S.
J. Biochem. 98, 1147-1156, 1985
A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylases deduced from the DNA sequences.
A;Reference number: A91997; MUID:86111694; PMID:2418011
A;Accession: A91997
A;Molecule type: DNA
A;Residues: 1-162, 'R', 164-512 <YU>
A;Cross-references: GB:X03236; NID:G39551; PIDN:CAA26981.1; PID:G39552
A;Experimental source: NCIB 27811
R;Gray, G.L.; Mainzer, S.E.; Ray, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: B24549
A;Molecule type: DNA
A;Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
A;Cross-references: GB:M13256; NID:G42510; PIDN:AAA22240.1; PID:G142511
A;Experimental source: NCIB 8061
R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, 369-372, 1984
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase gene
A;Reference number: A91796; MUID:84185455; PMID:6609154
A;Accession: A91796
A;Molecule type: DNA
A;Residues: 1-104 <STE>
A;Cross-references: GB:X01984; NID:G142432; PIDN:AAA22193.1; PID:G142433
R;Sibakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase gene
A;Reference number: A21663; MUID:85076654; PMID:6334606
A;Accession: A21663
A;Molecule type: DNA
A;Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 81-104, 'L', 106-110, 'G', 112-113, 'A', 115-116, 'G', 118-119, 'G', 121-122, 'G', 124-125, 'G', 127-128, 'G', 130-131, 'G', 133-134, 'G', 136-137, 'G', 139-140, 'G', 142-143, 'G', 145-146, 'G', 148-149, 'G', 151-152, 'G', 154-155, 'G', 157-158, 'G', 160-161, 'G', 163-164, 'G', 166-167, 'G', 169-170, 'G', 172-173, 'G', 175-176, 'G', 178-179, 'G', 181-182, 'G', 184-185, 'G', 187-188, 'G', 190-191, 'G', 193-194, 'G', 196-197, 'G', 199-200, 'G', 202-203, 'G', 205-206, 'G', 208-209, 'G', 211-212, 'G', 214-215, 'G', 217-218, 'G', 220-221, 'G', 223-224, 'G', 226-227, 'G', 229-230, 'G', 232-233, 'G', 235-236, 'G', 238-239, 'G', 241-242, 'G', 244-245, 'G', 247-248, 'G', 250-251, 'G', 253-254, 'G', 256-257, 'G', 259-260, 'G', 262-263, 'G', 265-266, 'G', 268-269, 'G', 271-272, 'G', 274-275, 'G', 277-278, 'G', 280-281, 'G', 283-284, 'G', 286-287, 'G', 289-290, 'G', 292-293, 'G', 295-296, 'G', 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Db 390 VFTGDMYG--TKGDSOREIPALKKHKIEPILKARKQYAYGAHQDYFDHHDIVGWTRGDSS 447

Qy 421 HPNSGLATIMSDGAGGSKMFWGNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480

Db 448 VANSGLAALITDGGGAKMYVGRQAGETWHDITGNRSEPVVINSGEWGEFHVNGGSVS 507

Qy 481 IWVWK 485

Db 508 IYVQR 512

RESULT 3

A54541

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI1792)

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C;Species: Bacillus stearothermophilus

C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997

C;Accession: A54541

R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.

FEMS Microbiol. Lett. 77, 271-276, 1991

A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.

A;Reference number: A54541

A;Accession: A54541

A;Molecule type: DNA

A;Residues: 1-549 <JOR>

A;Cross-references: GB:X59476

A;Experimental source: chromosomal DNA of strain DNI1792

C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the

C;Genetics:

A;Start codon: GTG

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-549/Product: alpha-amylase #status predicted <MAT>

F;235-368/Domain: alpha-amylase core homology <AMY>

F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.3%; Score 1874.5; DB 1; Length 549;

Best Local Similarity 67.2%; Pred. No. 1.3e-121;

Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;

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Db 39 NGTMMQYFEWYLPDDGTLWTKVANEANLSSGITALWLPAYKGTSDVGVGYDLYD 98

Qy 66 LGFBNQKGTVRTKGTGTSQLOAAVTSLNKNGIOVYGDVVMNHKGCADATEMVRVAVENPN 125

Db 99 LGFBNQKGTVRTKGTGTSQLOAAVTSLNKNGIOVYGDVVMNHKGCADATEMVRVAVENPN 158

Qy 126 NRNQEVGTGYTIEAWTFDFPFGNGTHSSFKRWYHFDGVDWDSRLNNRIYKFRGHGK 185

Db 159 DRNQEISGTYQIQAWTKDFPFGNGTYSFKRWYHFDGVDWDSRL--SRIYKFRGIGK 217

Qy 186 AWDWEVDTEGNDYLMYADIDMDHPVNVNELRWGVMYVNTLGLDGFRLDAVKHIKYSF 245

Db 218 AWDWEVDTEGNDYLMYADIDMDHPVNVNELRWGVMYVNTLGLDGFRLDAVKHIKFSF 277

Qy 246 TRDWINHVRSGATGKNMFAVEAFWKNDI-GAENYLOKTNWNSHVPDVLPHYLNLYNASKSGG 305

Db 278 FPDWLSVRSQTGKPLFTVGEIWSYDINKLHNYITKDTGWSLFDAPLHKNFTASKSGG 337

Qy 306 NYDMRNINFGTVQRHPSHVAFTVDNDSOPEEALESFVBWEKFLAYALTLTREOGYPS 365

Db 338 AFDMRLMTWTLMKDQTLTAVTFVDNHDTEPGALQSWDPWPFKFLAYAFILTEQGYPC 397

Qy 366 VFYGDYTGIPTHGVPMRSKIDPILAEARQYKQNDYLDHNNIIGWTRGNTAHNPSG 425

Db 398 VFYGDYTGIPQYNIPSLSKIDPLLIARRDYAGTQHDYLDHSDIIGWTRGGTEKPGSG 457

Qy 426 LATIMSDGAGGSKMFWGNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVSIVW 483

Db 458 LAALITDGGGSKMFWGNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVSIVW 515

RESULT 4

A24549

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C;Species: Bacillus stearothermophilus

C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

C;Accession: A24549; I39501; I39770

R;Gray, G.I.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt,

J. Bacteriol. 166, 635-643, 1986

A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearother

A;Reference number: A91817; MUID:86195857; PMID:3009417

A;Accession: A24549

A;Molecule type: DNA

A;Residues: 1-549 <GRA>

A;Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513

A;Experimental source: genomic DNA of strain NZ-3

R;Satoh, H.; Nishida, H.; Isono, K.

J. Bacteriol. 170, 1034-1040, 1988

A;Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distar

A;Reference number: I39501; MUID:88139156; PMID:3257753

A;Accession: I39501

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 536-549 <RES>

A;Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478

A;Experimental source: strain DY-5

A;Accession: I39770

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 536-549 <RE2>

A;Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486

A;Experimental source: strain 799

C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the

C;Genetics:

A;Start codon: GTG

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-549/Product: alpha-amylase #status predicted <MAT>

F;235-368/Domain: alpha-amylase core homology <AMY>

F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.1%; Score 1867.5; DB 1; Length 549;

Best Local Similarity 67.2%; Pred. No. 3.9e-121;

Matches 321; Conservative 75; Mismatches 81; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVIIPAWKAGSQNDVGVGAYDLYD 65

Db 39 NGTMMQYFEWYLPDDGTLWTKVANEANLSSGITALWLPAYKGTSDVGVGYDLYD 98

Qy 66 LGFBNQKGTVRTKGTGTSQLOAAVTSLNKNGIOVYGDVVMNHKGCADATEMVRVAVENPN 125

Db 99 LGFBNQKGTVRTKGTGTSQLOAAVTSLNKNGIOVYGDVVMNHKGCADATEMVRVAVENPN 158

Qy 126 NRNQEVGTGYTIEAWTFDFPFGNGTHSSFKRWYHFDGVDWDSRLNNRIYKFRGHGK 185

Db 159 DRNQEISGTYQIQAWTKDFPFGNGTYSFKRWYHFDGVDWDSRL--SRIYKFRGIGK 217

Qy 186 AWDWEVDTEGNDYLMYADIDMDHPVNVNELRWGVMYVNTLGLDGFRLDAVKHIKYSF 245

Db 218 AWDWEVDTEGNDYLMYADIDMDHPVNVNELRWGVMYVNTLGLDGFRLDAVKHIKFSF 277

Qy 246 TRDWINHVRSGATGKNMFAVEAFWKNDI-GAENYLOKTNWNSHVPDVLPHYLNLYNASKSGG 305

Db 278 FPDWLSYVRSGTQKPLFTVGEYMSYDINKLHNYYITKTNGTMSLFDAPLHNKFTASKSGG 337
QY 306 NYDMENIFNGTVQVRHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOQYPS 365
Db 338 AFDMSTLNNLTKMDQDTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAILTRQEGYPC 397
QY 366 VFYGDYGYGIPTHGVPMRMSKIDPILFARQYAYGKQNDYLDHNNIIGWTREGNTAHPSNG 425
Db 398 VFYGDYGYGIPQYNIPLSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKPGSG 457
QY 426 LATIMSDGAGSKMVFGRNKAQOWSDITGNRTGTVTINADGKNFNSVNGSVSIWV 483
Db 458 LAALITDGGSGKMWYVGQHAGKVFYDLTGNRSDDTVTINSOGKEFKVNGSGSVWV 515
RESULT 5
A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; I39777
R;Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Accession: A24436
A;Molecule type: DNA
A;Residues: 1-549 <NA>
A;Cross-references: GB:M11450
A;Experimental source: plasmid pAT5
A;Note: amino end of the mature protein also determined
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39777
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-45 <RES>
A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Gene: amyS
A;Genome: plasmid
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
F;1-34/Domain: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;35-549/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted
Query Match 69.1%; Score 1866.5; DB 1; Length 549;
Best Local Similarity 66.9%; Pred. No. 4.5e-121;
Matches 320; Conservative 75; Mismatches 82; Indels 1; Gaps 1;
QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAKWGASQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLTWKVANEANLNLSSGLITALLPAPKGTSSRDVGYGVYDLYD 98
QY 66 LGFBNQKGTVRTKGTSLQAAVTSLNKNGIQYGVGVVWNNHGGADATEMTRAVEVNPV 125
Db 99 LGFBNQKGAVRTKGTSLQAAVTSLNKNGIQYGVGVVWNNHGGADATEMTRAVEVNPV 158
QY 126 NRQEVTEGVTIBAWTRFDPFGNGTHSSPKRWYHFDGVDWQSRNLNRRNRYKFRGHGK 185
Db 159 DRNQETISGTTQIQAWTKFDFPGNGTYSFKNRWYHFDGVDWDESKL-SRIYKFRGIGK 217
QY 186 AMDWEVDTENGNYDLYMAYDIDMDHPVNVNLRNNGVWYNTNLGLDGRIDAVKHIKYSF 245

Db 218 AMDWEVDTENGNYDLYMAYDIDMDHPVNVNLRNNGVWYNTNLGLDGRIDAVKHIKYSF 277
QY 246 TRDWINHVSATCKNNFAVAEFWKNDLGALENVLOKTNHNSVFDYPLHNLNASKSGG 305
Db 278 FPDWLSYVRSGTQKPLFTVGEYMSYDINKLHNYYITKTNGTMSLFDAPLHNKFTASKSGG 337
QY 306 NYDMENIFNGTVQVRHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOQYPS 365
Db 338 AFDMSTLNNLTKMDQDTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAILTRQEGYPC 397
QY 366 VFYGDYGYGIPTHGVPMRMSKIDPILFARQYAYGKQNDYLDHNNIIGWTREGNTAHPSNG 425
Db 398 VFYGDYGYGIPQYNIPLSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKPGSG 457
QY 426 LATIMSDGAGSKMVFGRNKAQOWSDITGNRTGTVTINADGKNFNSVNGSVSIWV 483
Db 458 LAALITDGGSGKMWYVGQHAGKVFYDLTGNRSDDTVTINSOGKEFKVNGSGSVWV 515
RESULT 6
ALBSN
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amylioliquefaciens
C;Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A92389; I39763; I39763; A00843
R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
J. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced fr
A;Reference number: A92389; MUID:83108808; PMID:6185474
A;Contents: PUB110
A;Accession: A92389
A;Molecule type: DNA
A;Residues: 1-514 <TAK>
A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA221.
R;Chung, H.S.; Friedberg, P.
Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.
A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307
A;Molecule type: protein
A;Residues: 32-53, 'I', 55-63, 'L', 65-78, 'D', 80-83, 'S', 85-222 <CHU>
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A;Reference number: I39756; MUID:82051296; PMID:6170539
A;Accession: I39756
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.
Gene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its ow
A;Reference number: I39763; MUID:88137952; PMID:2830166
A;Accession: I39763
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-39 <RE2>
A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-362/Domain: alpha-amylase core homology <AMY>
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
Query Match 67.9%; Score 1836; DB 1; Length 514;

Db 302 GANYDLRGIFDTSLSVLEIKPDKAVTFVNDHDTQRCQALSTVEWFKPAPAYALILLRQDGL 361
Qy 364 PSVFGYDYGIP-THGVPAWMSKIDPILAEARQKAYGQNDYLDHNNIIGTWREGNTAHP 422
Db 362 PCVFGYDYGISGOYAQDFKILDRLLAIRKDLAYGEQNDYDFHANCIGWVRG--AEN 419
Qy 423 NSGLATMSDAGAGSKWFFVGRNKGAGQWSDITGNRTGTVTINADGWNFSVNGSGSVIW 482
Db 420 QSPITAVLISNDQENSKMFVQGEWTNTQTFVLLGSHQGVQVTEDEEGYQGFVPSARSVW 479
RESULT 11
AH2079
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-492 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073889.1; PID:gl7131281; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2190
C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
Query Match 47.2%; Score 1275; DB 2; Length 492;
Best Local Similarity 50.2%; Pred. No. 2.4e-80;
Matches 246; Conservative 72; Mismatches 156; Indels 16; Gaps 5;
Qy 6 NGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKG-ASQNDVGYGADLY 64
Db 5 NGTMQYFEWYLPNDGNLMSKVEASAPELADAGFTAWLPPAYKGPAGSDVGVGYDLP 64
Qy 65 DLGEFNQKGVTRTKYGRSLOQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRAVENP 124
Db 65 DLGEFDQKGVTRTKYGRQYLDVAKSLQTHGLQVYADAVLNHMKGGDAVETPKATFPQ 124
Qy 125 NNRQEVGTGYTTEATWTFDPGRCNTHSSFKRWYHFDGVDWDQSRLLNRIYKFRGHG 184
Db 125 DDRLNPKGGLQDKTYTHYFPGRQGYKSNFEMHWHFDDAVDYNEYS--GDRSTVYLLE 183
Qy 185 KAWDWEYDTENGNDYLYADIDMDHPEVNVNLRNKGWVYNTLGLDGFRIIDAVKHLYS 244
Db 184 KNFDYVALEKGNFAYLMGCDLDPQNEWVRGEVYWGKWLDTTKVDGFRIDAIKHISTW 243
Qy 245 FTRDWINHRSATGKNMFAVAFWKNLGAIENTYLOKTNMNHVSFVDFPLHLYNLSKSG 304
Db 244 FPEWIDALERHACKDLFMVGEYWNIDNTLLWTVDAVRGKMSVDFVPLHYNFHAQSKG 303
Qy 305 GNYDMRNIFNGTVVQRHPSHAFTVDNHDQPEALESFVEEWFKPLAYALTITREGQYP 364
Db 304 GNYDMRRLDGTMMQQRPTAVTFVNHDSQPLQALESVVEWFKPLAYAILLRQEGYP 363
Qy 365 SVFXYGDIYGPITHG-----VPAMRSKIDPILAEARQKAYGQNDYLDHNNIIGW 413
Db 364 CVFHADYIAGYEYDNGKGNRYNIFMPSHRWIIDKLKYARKHAYGPOYNLDHNTIGW 423
Qy 414 TREGNTAHPNSGLATIMSDGAGSKWFFVGRNKGAGQWSDITGNRTGTVTINADGWNFS 473
Db 424 TRLGDAHP-QCMVAVIMSDSGEIGKWEVG--KNTKFDILTHERIKAVYTNWEGWEFR 480
Qy 474 VNGSGSVIW 483
Db 481 CLGGSVSVW 490

RESULT 12

C86781

alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: C86781

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich,

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: C86781

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-491 <STO>

A:Cross-references: GB:AE005176; PID:gl2724224; PIDN:AAK05349.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: amyl

C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 42.1%; Score 1139; DB 2; Length 491;

Best Local Similarity 42.2%; Pred. No. 5.6e-71;

Matches 202; Conservative 101; Mismatches 172; Indels 4; Gaps 3;

Qy 8 TMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGAS-QNDVGYGADLYDL 66

Db 3 TILQAFWYLPSPSOHWNNIKENIPDLKLGFSGLWLPAPASKAASGVEDVGYGYDLPDL 62

Qy 67 GFNQKGVTRTKYGRSLOQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRAVENPNN 126

Db 63 GFQDKGTIPTKYGTGDEYLDLINTLHNNIEVYADVFNHMGADTETIEADIKAEKN 122

Qy 127 NRQEVGTGYTTEATWTFDPGRCNTHSSFKRWYHFDGVDWDQSRLLNRIYKFRGHGKA 186

Db 123 HLHNIENKNTVEWTKTFPFQRCQGYDNYITWHTFTGIDYDE-RKNQEEILEFEH--E 179

Qy 187 WDWEYDTENGNDYLYADIDMDHPEVNVNLRNKGWVYNTLGLDGFRIIDAVKHLYSFT 246

Db 180 WDENVSENNDFYLMGADLDFSVSEIVQEKWGHWFSEMTKIDGFRIDAKHIDFKYP 239

Qy 247 RDMINHRSATGKNMFAVAFWKNLGAIENTYLOKTNMNHVSFVDFPLHLYNLSKSGGN 306

Db 240 DKWLEQRAKQLDRKLFVGEVWSDDLGKLYLEQSSDRILQDFVPLHFNKKEASTNGE 299

Qy 307 YDMRNIFNGTVVQRHPSHAFTVDNHDQPEALESFVEEWFKPLAYALTITREGQYPSV 366

Db 300 FDMRTLFDHTLTASQPELSVTFVDNHDQRCQALQSWIPAWFKFEHAYSLILLRKKETPTV 359

Qy 367 FYGDIYGPITHGVPAMRSKIDPILAEARQKAYGQNDYLDHNNIIGTWREGNTAHPNSGL 426

Db 360 FWGLYGIPIHNNVNPVGNLRTMIALRKDSFURENDYFDHPDIIIGWNTILKIDNKYGL 419

Qy 427 ATIMSDGAGSKWFFVGRNKGAGQWSDITGNRTGTVTINADGWNFSVNGSGSVIWVK 485

Db 420 SCILTNKGGSKYMIIDKAYAGKYIDLFGHEHPITILDQNGGAEFYVNDGVSVMVDK 478
RESULT 13
G98247
cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacteri

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002

C:Accession: G98247

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: G98247

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-506 <KUR>

A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GNO0170
C;Genetics:
A;Gene: AGR L 1863
A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 41.6%; Score 1125; DB 2; Length 506;
Best Local Similarity 45.6%; Pred. No. 5.4e-70;
Matches 227; Conservative 77; Mismatches 170; Indels 24; Gaps 7;

QY 3 NGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVMIPPAAWGASON-DVGYGAY 61
DB 11 NMAGRTLLQFFHYYPDGGKLMSEVAEKAESLAKMGITDVMPLPAYKAAGGYSVGYDTY 70
QY 62 DLYDLGEFNGKQVTRTKYGRSOLQAAVTSLKNGIQVYGVVNNHKGADATAMVRAVE 121
DB 71 DLPDLGEFDQKGVATKYGDRAALEHAGKTLKNGIRVHDVNLNKKMGADAEKRVRR 130
QY 122 VNPNNRQEVVTGEYTTIAWTRFPPGGRNTHSSFKRWYHFDGVDW-----DQSRRLNN 175
DB 131 VNPDDRDIIDDEPPALAYTRFTPPGRNGKHSKFIWDLKCFSGVDHIEEPTEDGIFRLVN 190
QY 176 RIYKRGHKADEWEDVTENGNDYLMYADIDMDHPEVNNELRWGVYVNTTGLDGFRI 235
DB 191 EY----GDGE-WNEEVDQENGDFDLMGADVFRNRAVYELKYWGRWLSQVQVDGFR 245
QY 236 DAVKHIKYSTROWINHVRSATGKMFVAFKNDLGAENYLOKTNWNSHSDVDFPLHY 295
DB 246 DAAKHIPAFWRDVGWGHMRETVPDLFVVAEYHWPDLKSLYLELVDKQLMFLDVALHH 305
QY 296 NLNASKSGGNYDMRNIFNGTVQVHPSHVAFTVDNHDSDQPEALRSFVEEWKPLAYAL 355
DB 306 SFHDASKQGGDFMRSIFDGLSVSAVDPHVAITVDNHDTPQLQSLRAPVFPWPKLAYAI 365
QY 356 TLREQGYPSVYGYDYG--IPTHGVPAMRSKID-----PILEARQKYAYGKNDYL 405
DB 366 ILLREEGVPCVFPDLFGTSYTDGNDGNEYKIDIPALECLPKLIEARSFANGPQTDIF 425
QY 406 DHNIIGWTRGNTAHNSGLATIMSDGAGSKWMFVGRNKAGQVMSDITGNRTGTW 465
DB 426 DDASCTAFIRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHRHEHTLD 483
QY 466 ADGWNFSVNGGYSIWW 483
DB 484 ESGKGTPTNGGYSVWV 501

RESULT 14
AD3038
alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3038
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-495 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GNO0187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: amyA
A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 41.6%; Score 1124; DB 2; Length 495;

Best Local Similarity 45.8%; Pred. No. 6.1e-70;
Matches 226; Conservative 77; Mismatches 166; Indels 24; Gaps 7;

QY 8 TMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVMIPPAAWGASON-DVGYGAYDYL 66
DB 5 TLLQFFHYYPDGGKLMSEVAEKAESLAKMGITDVMPLPAYKAAGGYSVGYDTYDL 64
QY 67 GFNQKQVTRTKYGRSOLQAAVTSLKNGIQVYGVVNNHKGADATAMVRAVEVNN 126
DB 65 GFQDQKGVATKYGDRAALEHAGKTLKNGIRVHDVNLNKKMGADAEKRVRRVNP 124
QY 127 RQEVVTGEYTTIAWTRFDFPGRNTHSSFKRWYHFDGVDW-----DQSRRLNNRIYKF 180
DB 125 RTDIDDEPPALAYTRFTPPGRNGKHSKFIWDLKCFSGVDHIEEPTEDGIFRLVNE 181
QY 181 RGHGKAWDEWEDVTENGNDYLMYADIDMDHPEVNNELRWGVYVNTTGLDGFRI 240
DB 182 -GDGE-WNEEVDQENGDFDLMGADVFRNRAVYELKYWGRWLSQVQVDGFRDLAAKH 239
QY 241 IKYSFTRDWINHVRSATGKMFVAFKNDLGAENYLOKTNWNSHSDVDFPLHYNLNA 300
DB 240 IPAFWRDVGWGHMRETVPDLFVVAEYHWPDLKSLYLELVDKQLMFLDVALHHSF 299
QY 301 SKSGGNYDMRNIFNGTVQVHPSHVAFTVDNHDSDQPEALRSFVEEWKPLAYALTRE 360
DB 300 SKQGGDFMRSIFDGLSVSAVDPHVAITVDNHDTPQLQSLRAPVFPWPKLAYAILRE 359
QY 361 QGYPSVYGYDYG--IPTHGVPAMRSKID-----PILEARQKYAYGKNDYLDHNI 410
DB 360 EGVPCVFPDLFGTSYTDGNDGNEYKIDIPALECLPKLIEARSFANGPQTDIFDASC 419
QY 411 IGWTRGNTAHNSGLATIMSDGAGSKWMFVGRNKAGQVMSDITGNRTGTW 470
DB 420 IAFIRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHRHEHTLD 477
QY 471 NFSVNGGYSIWW 483
DB 478 TPTNGGYSVWV 490

RESULT 15
B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Salmonella typhimurium
C;Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: B45738
R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A;Reference number: A45738; MUID:93015717; PMID:1400215
A;Accession: B45738
A;Molecule type: DNA
A;Residues: 1-494 <RAH>
A;Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045
C;Genetics:
A;Gene: amyA
A;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F;202-335/Domain: alpha-amylase core homology <AMY>
F;239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.7%; Score 1074; DB 1; Length 494;
Best Local Similarity 43.1%; Pred. No. 1.7e-66;
Matches 212; Conservative 78; Mismatches 184; Indels 18; Gaps 6;

QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVMIPPAAWGASON-DVGYGAYDYL 64
DB 3 NPTLLQYFHYYPDGGKLMSELAERADGLNDIGINWVLPAPACKGASGGYSVGYDTYDLF 62


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QY 65 DLGEFNOKGTVRYKYGTRSQLAAVTSIKNGIOVYGDVWVNHKGGADATEMURAVEVNP 124
Db 63 DLGEFDQKGTATKYGDKRQLLTAIDALKKNIAVLLDVVWVNHKMGADAKERIRQVRVQ 122
QY 125 NNRNQEVGTTEATWTRFDPGGRNTHSSGFKWYHFDGVDWDSRRLANNRIYKFRGH- 183
Db 123 DDTQIDDDNIIECEGWTRYTFPARAQYSFIWDYHCFSGIDHIEFDP-EDGIFKIVNDY 181
QY 184 -GKAWDEVTENGNYDYLADIDMDHPEVNVNLRNMGVYNTLGLDGFRIIDAVRHK 242
Db 182 TGDGWNQVDDMGNFYLMGENIDFRNHAVTEBIKYWARVWMEQTHCDGFRIDAVRHP 241
QY 243 YSFTRDWNVRSNTGKMFVAFKNDLGAENYLOKTNWNSVFDVPLHYNLYNASK 302
Db 242 AWFYKEWIEHVQAVAPKPLFIVAEYWSHEVDKLTQYIDQVDGKTMFLDAPLQMKFHEASR 301
QY 303 SGGNYDMRNIFNGTVVORHPSHAVTFVDNHDSDPEEALSFVREWFKPLAYALTLTREQ 362
Db 302 QGAEYDMRHIFTGLVEADPFHAVTLVANHDTQPLQALEAPVEPWFKPLAYALTLLRENG 361
QY 363 YPSVFGDYGYGIPTH-----GVPAMRSKIDPILBAROKYAYGKQNDYLDHNNII 411
Db 362 VPSVFYFDLYGASVEDSGENGETCRVDMPIV-NQLDRLLILARQRFAGIQTLFFDHNCI 420
QY 412 GWTREGNTAHPNSGLATIMSDGAGSKWMFVGRNKAGQVMSDITGNRTGTVTINADGWN 471
Db 421 AFSRSGTEENP--GCVVVLSNGDDGKTKLLLDGNYANKTWDRDFSGNRDEYVVTNDQGEAT 478
QY 472 FSVNGGSVSIWV 483
Db 479 FFCNAGSVSVWV 490

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Search completed: October 7, 2004, 00:20:49
 Job time : 15.886 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.50628 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-13

Perfect score: 2703

Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGNGNFSVNGSVSIWVWK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	518	1 AMT6_BACS7	P19571 bacillus sp
2	1876	69.4	512	1 AMY_BACLI	P06278 bacillus li
3	1866.5	69.1	549	1 AMY_BACST	P06279 bacillus st
4	1836	67.9	514	1 AMY_BACAM	P00692 bacillus am
5	1072	39.7	494	1 AMY2_SALTY	P26613 salmonella
6	1045	38.7	495	1 AMY2_ECOLI	P26612 escherichia
7	331	12.2	1196	1 AMYB_PAEPO	P21543 paenibacill
8	281.5	10.4	421	1 AMYA_VIGMU	P17859 vigna mungo
9	276	10.2	440	1 AM3A_ORYSA	P27932 oryza sativ
10	265	9.8	437	1 AM3C_ORYSA	P27939 oryza sativ
11	265	9.8	438	1 AM3B_ORYSA	P27937 oryza sativ
12	264.5	9.8	435	1 AM3D_ORYSA	P27933 oryza sativ
13	263.5	9.7	551	1 AMT4_PSESA	P22963 pseudomonas
14	260	9.6	368	1 AMY3_HORVU	P04747 hordeum vul
15	259	9.6	548	1 AMT4_PSSST	P13507 pseudomonas
16	258	9.5	427	1 AMY2_HORVU	P04063 hordeum vul
17	258	9.5	429	1 AMY6_HORVU	P04750 hordeum vul
18	255	9.4	413	1 AMY3_WHEAT	P08117 triticum ae
19	254	9.4	719	1 AMY1_BACST	P19531 bacillus st
20	253.5	9.4	498	1 AMYA_ASAPW	Q02905 aspergillus
21	253.5	9.4	499	1 AMYB_ASAPW	Q02906 aspergillus
22	252.5	9.3	428	1 AMY1_ORYSA	P27654 oryza sativ
23	252.5	9.3	499	1 AMYA_ASPOH	P10529 aspergillus
24	251.5	9.3	499	1 AMYB_ASPOH	P30292 aspergillus
25	250	9.2	437	1 AM3E_ORYSA	P27934 oryza sativ
26	248	9.2	713	1 CDGT_BACSP	P30921 bacillus sp
27	247.5	9.2	438	1 AMY1_HORVU	P00693 hordeum vul
28	247.5	9.2	718	1 CDGT_BACCI	P30920 bacillus ci
29	246.5	9.1	713	1 CDGT_PAEWA	P31835 paenibacill
30	245.5	9.1	710	1 CDGT_THETU	P26827 thermocanaer
31	244	9.0	712	1 CDGT_BACS3	P09121 bacillus sp
32	240.5	8.9	718	1 CDGT_BACSS	P31747 bacillus sp
33	240	8.9	713	1 CDGT_BACS8	P27692 bacillus sp

34	238	8.8	528	1 AMY_BACCI	P08137 bacillus ci
35	235	8.7	713	1 CDGT_BACCI	P43379 bacillus ci
36	234	8.7	713	1 CDGT_BACSO	P05618 bacillus sp
37	229	8.5	494	1 AMY1_SACFI	P21567 saccharomyc
38	228.5	8.5	442	1 MGTA_THENE	O86956 thermotoga
39	226.5	8.4	718	1 CDGT_BACLI	P14014 bacillus li
40	221.5	8.2	443	1 AMC2_ORYSA	P27935 oryza sativ
41	221.5	8.2	445	1 AMC2_ORYSA	P27941 oryza sativ
42	221	8.2	703	1 CDGT_BACS2	P31746 bacillus sp
43	220	8.1	564	1 AMY4_SCHPO	O94789 schizosach
44	219.5	8.1	711	1 CDGT_BACST	P31797 bacillus st
45	213.5	7.9	441	1 MGTA_THENA	P80099 thermotoga

ALIGNMENTS

RESULT 1

AMT6_BACS7

ID AMT6_BACS7 STANDARD; PRT; 518 AA.

AC P19571;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amyase)

DE (Maltohexaosase-producing amylase) (Exo-maltohexaohydrolase).

OS Bacillus sp. (strain 707)

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

ON NCBI_TaxID=1416;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.

RX MEDLINE=88162814; PubMed=3258152;

RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;

RT "Nucleotide sequence of the maltohexaosase-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to

RT liquefying type alpha-amyloses.";

RL Biochem. Biophys. Res. Commun. 151:25-31(1988).

CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive

CC maltohexaosase residues from the non-reducing chain ends.

CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By

CC similarity).

CC -1- PATHWAY: Starch degradation.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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EMBL; M18862; AAA22231.1; --

DR PIR; A27705; A27705.

DR HSP; P06278; 1VUS.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amyase; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR SMART; SM00642; Amy; 1.

DR Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.

FT SIGNAL 1 33

FT CHAIN 34 518 GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.

FT ACT_SITE 269 269 BY SIMILARITY.

FT ACT_SITE 273 273 BY SIMILARITY.

FT ACT_SITE 366 366 BY SIMILARITY.

FT METAL 139 139 CALCIUM 1 (BY SIMILARITY).

FT METAL 196 196 CALCIUM 2 AND SODIUM (BY SIMILARITY).

FT METAL 219 219 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY

FT METAL 219 219 SIMILARITY).

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FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 240 240 CALCIUM 2 (BY SIMILARITY).
FT METAL 242 242 CALCIUM 2 (BY SIMILARITY).
FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
Query Match 100.0%; Score 2703; DB 1; Length 518;
Best Local Similarity 100.0%; Pred. No. 8.4e-178;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 60
Db 34 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 93
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLOQAATVSLKNGGIQVYGDVVMNHKGGADATEMVRV 120
Db 94 YDLYDLGEFNQKGTVRTKYGTRSQLOQAATVSLKNGGIQVYGDVVMNHKGGADATEMVRV 153
QY 121 EVNPNRNQEVGTGEYTIETAWTRDFPGRGNTSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
Db 154 EVNPNRNQEVGTGEYTIETAWTRDFPGRGNTSSFKRWYHFDGVDMDQSRRLNNRIYKF 213
QY 181 RHGKAWDEVDTEGNYDYLMTADMDHPVWNLNRKGVWYVYTLGLDGRIDA VKH 240
Db 214 RHGKAWDEVDTEGNYDYLMTADMDHPVWNLNRKGVWYVYTLGLDGRIDA VKH 273
QY 241 IKYSPTRDWLNHVRSATGKNMFAVEFKNDLGAENLYLQKTNWNSVFDVPLHYNLNNA 300
Db 274 IKYSPTRDWLNHVRSATGKNMFAVEFKNDLGAENLYLQKTNWNSVFDVPLHYNLNNA 333
QY 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTITRE 360
Db 334 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTITRE 393
QY 361 QGYPSVPYGYGYPITHGVPAWMSKIDPILAEAKQYAYGKQNDYLDHNNIIGWTRGNTA 420
Db 394 QGYPSVPYGYGYPITHGVPAWMSKIDPILAEAKQYAYGKQNDYLDHNNIIGWTRGNTA 453
QY 421 HPNSGLATIMSDGAGSKWPFVGRNKGQYVSDITGNRTCTGTVTINADGWNFSVNGGSVS 480
Db 454 HPNSGLATIMSDGAGSKWPFVGRNKGQYVSDITGNRTCTGTVTINADGWNFSVNGGSVS 513
QY 481 IWVWK 485
Db 514 IWVWK 518
RESULT 2
AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (BLA).
GN AMYS OR AMYL.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=8611694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amylases
RT deduced from the DNA sequences."
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RL J. Biochem. 98:1147-1156 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Shahhosseini M., Ziaei A.A., Ghaemi N., Pourbabaei A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372 (1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Laoidi B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442 (1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373 (1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2192788; PubMed=11997021;
RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltooligosaccharide substrates.";
RL FEBS Lett. 518:79-82 (2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RC STRAIN=ATCC 6598;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Gaillardin C., Masson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488 (1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037 (1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
RP AND GLU-365.
RC STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057 (2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
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RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Gaillardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RL modulation of its stability over a 50 degrees C temperature range.";
RL Protein Eng. 16:287-293(2003).
RP [12]
RN MUTAGENESIS OF TRP-292 AND VAL-315.
RP STRAIN=ATCC 27811;
RC MEDLINE=22797417; PubMed=12915728;
RX Rivera M.H., Lopez-Muncua A., Soberon X., Saab-Rincon G.;
RA "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycosylation
RT activity";
RL Protein Eng. 16:505-514(2003).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=ATCC 27811;
RX MEDLINE=95182462; PubMed=7877175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RL amylase at 2.2-A resolution.";
RL J. Mol. Biol. 246:545-559(1995).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98212915; PubMed=9551551;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Activation of Bacillus licheniformis alpha-amylase through a
RL disorder-->order transition of the substrate-binding site mediated
RL by a calcium-sodium-calcium metal triad.";
RL Structure 6:281-292(1998).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.
RL High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
RH62V/N219F/A238V/Q293S/N294Y.
RX STRAIN=ATCC 6598;
RC MEDLINE=22538505; PubMed=12540849;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
RL introduction of hydrophobic residues at the surface.";
RL J. Biol. Chem. 278:11546-11553(2003).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -!- SUBUNIT: Monomer.
CC -!- BIOTECHNOLOGY: Used in the food industry for high temperature
CC liquefaction of starch-containing mashes and in the detergent
CC industry to remove starch. Sold under the name Termamyl by
CC Novozymes.
CC -!- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
CC values (up to pH 11) and at high temperatures (up to 100 degrees
CC Celsius).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements> or
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X03236; CAA26981.1; -;
DR EMBL; M38570; AAA22226.1; -;
DR EMBL; M13256; AAA22240.1; -;
DR EMBL; K01984; AAA22193.1; -;

DR EMBL; AF438149; AA026743.1; -;
DR EMBL; M26412; AAA22237.1; -;
DR EMBL; A17930; CAA01355.1; -;
DR PIR; A91997; ALBSL.
DR PDB; 1BLI; 23-MAR-99.
DR PDB; 1BPL; 17-AUG-96.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR PDB; 1OB0; 03-APR-03.
DR PDB; 1VUS; 12-MAR-97.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 512
FT ACT_SITE 260 260
FT ACT_SITE 264 264
FT ACT_SITE 357 357
FT METAL 133 133
FT METAL 190 190
FT METAL 210 210
FT METAL 212 212
FT METAL 223 223
FT METAL 229 229
FT METAL 231 231
FT METAL 233 233
Query Match 69.4%; Score 1876; DB 1; Length 512;
Best Local Similarity 67.8%; Pred. No. 3.3e-121;
Matches 329; Conservative 66; Mismatches 80; Indels 10; Gaps 4;
QY 6 NGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKGSQNDVGYGAYDLYD 65
DB 33 NGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKGSQNDVGYGAYDLYD 92
QY 66 LGFEFNQKGTVRTKYGTRSQLQAQAVTSLKNGIQYGVDMVNMHKGADATEMRAVEVNP 125
DB 93 LGFEFHQKGTVRTKYGTRSQLQAQAVTSLKNGIQYGVDMVNMHKGADATEMRAVEVNP 152
QY 126 NRNEQVTEYTIETAWTRPDPFGRCNTHSSFKWRWYHFDGVDMQSRRLNNRIYKRGHK 185
DB 153 DRNEVISGEHRIKAWTHFFPGRGSTYSDFKWYHFDGTDWDSRKL-NRIYKFPQ--GK 209
QY 186 AWDHEVDTEGNDYLMYADIDMDHPVNMELRNWGVYNTLTGLDGFRIIDAVKHYSF 245
DB 210 AWDHEVSENGNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVXHKFSF 269
QY 246 TRDWINVRSATGKNMFAVAFWKNLGAENYLYQKNWNHVSFDPVPLHYNLNASKSGG 305
DB 270 LRDMVNVHRETKEMFTVAEYQNDLGALENLYNKNFNHVSFDPVPLHYQFHAASQGG 329
QY 306 NYDMRNTFNGTVQVRHPSHAVTFVDNHDSPQEALESFVEEWFKPLAYALTLTREQGYPS 365
DB 330 GYDMKRLNLSVSKHPLKAVTFVDNHDTPQGSLESTVQTFWFKPLAYALTLTREQGYPP 389
QY 366 VFYGDYGIPTHG-----VPAMRSKIDPILAEARKYAYGKQNDYLDHNNIGTWREGNTA 420
DB 390 VFYGDYMGY--TKGDSQREIPALKEIPILKARKYAYGAQHDFDHDHIDVGMVREGDSS 447
QY 421 HPNSGLATIMSDGAGGSKMFWGVGRNKGAGQVMSDITGNRTGTVTINADGWGNSFVNGGSVS 480
DB 448 VANSGLAALITDGPGRKRVTVGRQNAAGETWHIDITGNRSEPVVINSSEGNFHVNGGSVS 507
QY 481 IWNK 485
DB 508 IYVQ 512

```
RESULT 3
AMY_BACST
ID_ AMY_BACST STANDARD; PRT; 549 AA.
AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
GN glucanohydrolase).
OS AMYS.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=85234394; PubMed=3924897;
RA Nakajima R., Imanaka T., Aiba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
gene.";
RL J. Bacteriol. 163:401-406(1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DY5/PHI300;
RX MEDLINE=86008166; PubMed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Udaoka S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
homology between prokaryotic and eukaryotic alpha-amylases at the
active sites.";
RL J. Biochem. 98:95-103(1985).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3;
RX MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindler K.L.,
Carmona C., Reguadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P.;
RT "Thermotable alpha amylase of Bacillus stearothermophilus: cloning,
expression, and secretion by Escherichia coli.";
RL (In) Chaloupka J., Krumphanz V. (eds.);
EX Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RC STRAIN=DY-5;
RX MEDLINE=86059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
Idota Y., Yamagata H., Udaoka S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
protein-producing Bacillus brevis 47 carrying the Bacillus
stearothermophilus amylase gene";
RL J. Bacteriol. 164:1182-1187(1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21125602; PubMed=11226887;
RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:
possible factors determining the thermostability.";
RL J. Biochem. 129:461-468(2001).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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Db 421 AFSRSGTEHP--CCVVVLSNGDDGKTKLLGDNVANKTWKTRDFLGNRDEYVVTNDQGEAT 478
Qy 472 FSVNGGVSIVW 483
Db 479 FFCNAGSVSVW 490

RESULT 6
ID AMY2 ECOLI
AM2_1 AMY2 ECOLI STANDARD; PRT; 495 AA.
AC P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KJ2 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=KJ2;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayaashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIA and IIIB, including a
RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; L01642; AAA23810.1; -.
CC EMBL; AE000285; AAC74994.1; -.
CC EMBL; D90833; BAA15755.1; -.
CC EMBL; M85240; -, NOT ANNOTATED_CDS.
CC EMBL; L13279; AAA82575.1; -.
CC EMBL; D64956; AA5738.
CC HSP; P06278; IYUS.
CC Ecogene; EG11387; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Complete proteome.
CC ACT_SITE 235 235 BY SIMILARITY.
CC ACT_SITE 265 265 BY SIMILARITY.
CC ACT_SITE 332 332 BY SIMILARITY.
CC METAL 104 104 CALCIUM (BY SIMILARITY).
CC METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC CONFLICT 19 20 KL -> SS (IN REF. 1).
CC CONFLICT 109 109 A -> V (IN REF. 1).
CC CONFLICT 149 149 Q -> E (IN REF. 1).
CC CONFLICT 234 234 L -> I (IN REF. 1).
CC SEQUENCE 495 AA; 56639 MW; 2eAFF6797DDA54D6 CRC64;
Qy 6 NGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVIPPAWKAGSQN-DVGVGADLY 64
Db 3 NPTLLQCFHWYYPEGGKLPALAEADGPNIDGINMVLPPAYKAGSGYSGVSDYDLF 62
Qy 65 DLGEFNQKGVTRKYGTRSQLOQAATSLKNGQVGVGVVNMHKGADATEMVRAVNP 124
Db 63 DLGEFDQKGSIPTRYGDKAQLAALDAIKENDIAVLDDVVVNMHKGADAEKAIKRVQVNA 122
Qy 125 NNRNQEVTEGYTTEAATRFDPFGCRNTHSSFKRWYHFDGVDMQSRRLNNRIYKFRGH- 183
Db 123 DDRQTDEEIIIECEGWTRYTFPARAQYQSQFIWDFKCFSGIDHIENPD-EDGIFKIVNDY 181
Qy 184 -GKAWDEVTENGNDYLMYADIMDHPVFNELRNWGVVYNTLTGLDGRIDAVKHK 242
Db 182 TGEWNDQVDELGNFDYLMGENIDFRNHAIVTEIKYARWVMEQTCDCGFRLDVAKHIP 241
Qy 243 YSFTRDMINVRSATGKMEFAVEAFKNDLGAENIYKQTNWHSVDFDPLHLYNLVASK 302
Db 242 AMFYKEWIEHVQEVAPKPLFVAVYSHVSDVQKQTYIDQVEGKTMDFDPLQMKFHSAR 301
Qy 303 SGGNYDMRNIPNGTVQVORHPSHVAFTVDNHDSPPEALESFVEWFKPLAYALTLTREOG 362
Db 302 MGRDYMTQIPTGTLVEADPFHVAITLVANHDTPQLALEAPVPEWFPFLAYALLIRENG 361
Qy 363 YPSVYFYDYYGIPTHGVPA-----MRSKIDPILFARQKYAYQKNDYLDHNNIIG 412
Db 362 VPSVYFDLYGAHYEDVGGDQTYPIDMPIIEQLDELILARQFAHGVTQLFFDHPNCIA 421
Qy 413 WTRGNTAHNPNSGLATITMSDGAGSKMFMVGRNKAQGVWSDITGNRTGTVINADHGWNF 472
Db 422 FSRSGTDEFP--GCVVVMNSGDDGKTKLLGDNVANKTWKTRDFLGNRDEYVVTNDQGEATF 479

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Query Match 38.7%; Score 1045; DB 1; Length 495;
 Best Local Similarity 42.6%; Pred. No. 2.3e-64;
 Matches 209; Conservative 74; Mismatches 192; Indels 16; Gaps 5;

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QY 473 SVNGSVSIWV 483
Db 480 FCNGSVSVWV 490

RESULT 7
ID _AMVB PAEPO STANDARD; PRT; 1196 AA.
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amylase precursor [inclusion: Beta-amylase (EC 3.2.1.2)];
DE Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Straesser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amylase.";
RL Biochemistry 30:4594-4599(1991).
CC -I- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
CC SECRETION.
CC -I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -I- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M15817; AAA85446.1; -.
CC EMBL; Y00150; CAA68344.1; -.

DR PIR; A29130; A29130.
DR HSSP; P36924; 1B9Z.
DR InterPro; IPR006589; Alp_amyl_cat sub.
DR InterPro; IPR006048; Alpha_amyl_C_
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR005085; CBM_25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR001554; Glyco_hydro_14.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF03423; CBM_25; 2.
DR Pfam; PF01373; Glyco_hydro_14; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRINTS; PR00750; BETAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
DR PROSITE; PS00506; BETA_AMYLASE_1; 1.
DR PROSITE; PS00679; BETA_AMYLASE_2; 1.
DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
FT DOMAIN 36 454 BETA-AMYLASE.
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196
FT DISULFID 118 126
FT ACT_SITE 198 198
FT ACT_SITE 394 394
FT MUTAGEN 118 118
FT MUTAGEN 126 126
FT MUTAGEN 358 358
FT CONFLICT 1 1
FT CONFLICT 67 67
FT CONFLICT 100 100
FT CONFLICT 154 154
FT CONFLICT 177 177
FT CONFLICT 227 228
FT CONFLICT 330 330
FT CONFLICT 425 425
FT CONFLICT 493 493
FT CONFLICT 532 532
FT CONFLICT 559 559
FT CONFLICT 665 665
FT CONFLICT 681 681
FT CONFLICT 686 686
FT CONFLICT 725 728
FT CONFLICT 736 736
FT CONFLICT 741 741
FT CONFLICT 758 758
FT SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;

Query Match 12.2%; Score 331; DB 1; Length 1196;
Best Local Similarity 23.7%; Pred. No. 5e-15;
Matches 123; Conservative 70; Mismatches 188; Indels 138; Gaps 24;

QY 1 HINGTGTMMQVPEWYLPNDGNHNRNSDASNLKSGITAVWIPPAWKGASQNDV-GYG 59
Db 766 NYCGFNNSDQKWH-----GGDFQGIINKLDYIKMGFTAIWITPTVMQKSEVAYGHY 821
QY 60 AYDLYDLGFBFNGQGTVRTKYGTRSGQAQAVTSLKNNGIQYGVVNVNHHKGGADATEMVR 119
Db 822 TYDFY-----AVDGLHGTMDKLQELVRKAHDKNIAWVVDVNVNHTG----- 862
QY 120 VEVPNNRNVQVETGETIEAWTFDF-PRGNTHSSP-KRWVYHFGVDWDQSRNNRI 177
Db 863 -----DFQPGNGFAKAPFDKADWYHHNGDITDGDYNSNNQ- 897
QY 178 YKFRGHGKAWDMEDVDTEGNYDYLMTYADIDMDHPEVNVNLRNMGVYNTLTGLDGRIDA 237
Db 898 -----WKI--ENG--DVAGLDDLHNHENPATANELKWIKNLLNETGIDGLRLDT 942
QY 238 VKHIKYSFTRDWINHVRSATGKRMFAVEFWKNDLGAENLYLQKTNWNSHVFDFPLHYNL 297

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Db 943 VKHVPKFLKDF-----DQANTFTTGEIFHGPDPAYVGDY---TRYLDAALDFPMYTI 993
QY 298 YNASKSGGNDMRNIFNGTVVQHPHSHAVT---FVDNHDSPQBEALSFV-----344
Db 994 KDV--FGHDSMRKIDKDRYDRQATNGVFIDNHD-----VRFNDASGKPGAN 1045
QY 345 -EWFK-PLAYALTLTREOQVPSVFGYDYGIPTGHPVPMRSKIDPILFARQKAYGKQN 402
Db 1046 YDKWPQLKAALGFTLT-SRGIPIYQTEQYSGGDDPANRENN-----FNANH 1094
QY 403 DYLDHNNIIGTREGTAHPNSGLATTMSDAGSGKWM-----FVGRNKAG-----Q. 449
Db 1095 DLVQYIAKLNVRRN---HP-----ALQNGSQREKWDVDSFYFSQKNGKDEAIVFINN 1145
QY 450 VMSDIT---GN---RTGVTINADGNGFNSVNGGVSU 481
Db 1146 SWSQTFITGNFNLNGTLTNQLSNDSVQINNGSITV 1184

RESULT 8
AMYA VIGMU STANDARD; PRT; 421 AA.
ID AMYA VIGMU STANDARD; PRT; 421 AA.
AC P17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (Black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RT "Nucleotide sequence of cDNA for alpha-amylase from cotyledons of
RT germinating Vigna mungo seeds.";
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
RL Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC -----
CC ENBL; X53049; CAA37217.1; -.
CC DR ENBL; X73301; CAA51734.1; -.
CC DR PIR; S10514; S10514.
CC DR HSSP; P04063; IAVA.
CC DR InterPro; IPR006589; Alp amyl cat sub.
CC DR InterPro; IPR006047; Alpha amyl cat.
CC DR InterPro; IPR006046; Glyco_hydro_13.
CC DR Pfam; PF00128; alpha-amylase; 1.
CC DR PRINTS; PR00110; ALPHAAMYLASE.
CC DR SMART; SM00642; Amy1.

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KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT CHAIN 1 23 PROBABLE.
FT ACT_SITE 24 421 ALPHA-AMYLASE.
FT ACT_SITE 201 201 BY SIMILARITY.
FT METAL 113 113 BY SIMILARITY.
FT METAL 130 130 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 170 170 SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;

Query Match 10.4%; Score 281.5; DB 1; Length 421;
Best Local Similarity 25.3%; Pred. No. 3.4e-12;
Matches 98; Conservative 56; Mismatches 144; Indels 89; Gaps 15;

QY 9 MMQYFEWYLPNDGNHNRINSASNLKSGITAVWIPPAKMGASQNDVGYGAYDYLGE 68
Db 26 LFQGFNWESSKKGWYNSLKNIPDLANAGITHVWLPPPSQSVSPR--GYLPGLYDLD- 82
QY 69 FNQKGTVRTKYTRSQLOAAVTSLNKNGIOVYGVVNMHKGADATEWRAVEVNPNNRN 128
Db 83 -----ASKYGSKNELSLIAAFHEKGIKCLADIVINHR-----TAER 119
QY 129 QEVGYTIEAWTRFDPPFRGNTHSSPKRWYHFDGVDWDQSRRLNNRIYKFRGHKAWD 188
Db 120 KDGRIYCI-----FE-----GGTPDSRQ-----DWGSPFCRD-----D 149
QY 189 WEVDTEGNYD-----YLMYADIDMDHPEVNELENNWGVYNTLGLDGFIDAVKHKYS 244
Db 150 TAYSDGTGNNDSGEGYDAAPDIDHLNPOVQRELSMMNWLKTEIGFGWRFDFVKGYAPS 209
QY 245 FTRDWINHVRSAUCKNNPFAVEFW-----KNDLCAIENYLQKTNWNSHVF 289
Db 210 ISKIYMEQT-----KPDFAVGEKWDSSYQDGKPNYQDSHRGALVNWVESAGAITAF 264
QY 290 DVPLHLYNLNASKSGGNYDMRNIFNGT---VVRHPSHAYTFVDNHDSPQBEALSF-VE 345
Db 265 DFTTK-GILQAAVQGLWRLIDP-NGKPPGMIGVKPENAVTFIDNHDGTSTQRLWPFPSD 322
QY 346 EWFKPLAYALTLTREOQVPSVFGYDY 372
Db 323 KVMQGVAYILT---HPGTSPSIFYDHF 346

RESULT 9
AM3A ORYSA STANDARD; PRT; 440 AA.
ID AM3A ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etioolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).

```


FT METAL 153 CALCULUM 3 (BY SIMILARITY).
 FT METAL 164 CALCULUM 3 (BY SIMILARITY).
 FT METAL 167 CALCULUM 3 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).
 FT METAL 168 CALCULUM 1 (BY SIMILARITY).
 FT METAL 169 CALCULUM 1 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).
 FT METAL 172 CALCULUM 3 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).
 FT METAL 174 CALCULUM 1 AND 3 (BY SIMILARITY).
 SQ SEQUENCE 437 AA; 48637 MW; BD304250B40C7A8B CRC64;

Query Match 9.8%; Score 265; DB 1; Length 437;
 Best Local Similarity 23.7%; Pred. No. 4.9e-11;
 Matches 109; Conservative 57; Mismatches 155; Indels 138; Gaps 21;

Qy 9 MMQYFEWYLPN-DGNHWNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGAYDLYDLG 67
 Db 29 LFOGFNWSWKQGGWYNFLSHVDYIAATGVTHVWLPSPSHVAPQ--GYMPGRLYDL 86
 Qy 68 EFNQGTVRTKYTRSQQAQAVTSLKNGIQVYGDVNNHKGADATEMVRVAVENPNR 127
 Db 87 -----ASKYGTGAELSLIAAFHSKSIKCVADIVINHR-CAD----- 122
 Qy 128 NOEVTGTYTIAWTRFPFGNTHSSFKWYHFDGVDW---DQSRRLNNRIYKFRGHG 184
 Db 123 YKDSRGYICI-----PEG-GTPDSRLDW-----GPDMTCSDDTQYSNG--RGH- 162
 Qy 185 KAWDEVDTENGNYDYLMYADIDMDHPEVNNELRWGYYNTLGLDFRIDAVKHYS 244
 Db 163 -----RTGADFGAAPDIDLHNTVQELSDFNLWLNKSDVDFGWRDLDFAKYSAT 213
 Qy 245 FTRDWINHVSATGNMFAVAFWKN-----DLGAIENYLOKTNWHSVF 289
 Db 214 VAKTYVDNTPS-----FVVAEISWNRDYGNGBPSSWQDGRQELYNVAQVGPASAF 268
 Qy 290 DVPLHNYLNASKGNGVDMNINFGT---VVQRHPSHAVTFVNDHDSQPEALESF-VE 345
 Db 269 DFTTKGEL-QAAQOGLWRMD-GNGKAPGMIGLPEKAVTFIDNHDGTSTQNSWPPSPD 326
 Qy 346 ENFKPLAYALTLTREQGVPSPYGYGIPHTGVPMARSKIDPILBARQYAYGKQNDYL 405
 Db 327 KVMQRYAYILT---HPGVPCIFY----- 346
 Qy 406 DHNNIIGW-----TREGNTAHNSGLATIMSDG 433
 Db 347 DH--VFDWNLKQEIISTLAAVRSRNGIHPGSKNIIAADG 383

RESULT 11
 AM3B ORYSA
 ID AM3B ORYSA STANDARD; PRT; 438 AA.
 AC P27937;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 glucanohydrolase).
 GN AM1.6 OR AM13B.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica M202; TISSUE=Etolated leaf;
 RX MEDLINE=91329692; PubMed=1714318;
 RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
 RL "Characterization of an alpha-amylase multigene cluster in rice.";
 RN Plant Mol. Biol. 16:579-591 (1991).
 RP SEQUENCE FROM N.A.

RA Sutliff T.D., Huang N., Rodriguez R.L.;
 RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
 CC FUNCTION: Important for breakdown of endosperm starch during
 germination.
 CC CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC SUBUNIT: Monomer.
 CC TISSUE SPECIFICITY: Germinating seeds.
 CC DEVELOPMENTAL STAGE: Expressed at a high level during germination
 in the aleurones cells under the control of the plant hormone
 gibberellic acid and in the developing grains at a low level.
 CC SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 or send an email to license@isb-sib.ch).
 DR EMBL; X56337; CAA39777.1; -;
 DR EMBL; M24941; AAA33897.1; -;
 DR PIR; S14957; S14957.
 DR HSSP; P04063; IAVA.
 DR Gramene; P27937; -;
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27 438
 FT ACT_SITE 205 205
 FT ACT_SITE 313 313
 FT METAL 117 117
 FT METAL 134 134
 FT METAL 137 137
 FT METAL 139 139
 FT METAL 143 143
 FT METAL 153 153
 FT METAL 164 164
 FT METAL 167 167
 FT METAL 168 168
 FT METAL 169 169
 FT METAL 172 172
 FT METAL 174 174
 SQ SEQUENCE 438 AA; 48591 MW; B9DE0DB5ABC63F9C CRC64;

Query Match 9.8%; Score 265; DB 1; Length 438;
 Best Local Similarity 23.5%; Pred. No. 4.9e-11;
 Matches 109; Conservative 55; Mismatches 153; Indels 146; Gaps 22;

Qy 9 MMQYFEWYLPNDGNHWNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGAYDLYDLG 67
 Db 29 LFOGFNWSWKQGGWYNFLSHVDYIAATGVTHVWLPSPSHVAPQ--GYMPGRLYDL 86
 Qy 68 EFNQGTVRTKYTRSQQAQAVTSLKNGIQVYGDVNNHKGADATEMVRVAVENPNR 127
 Db 87 -----ASKYGTGAELSLIAAFHSKSIKCVADIVINHR-CAD----- 122
 Qy 128 NOEVTGTYTIAWTRFPFGNTHSSFKWYHFDGVDW---DQSRRLNNRIYKFRGHG 184
 Db 123 YKDSRGYICI-----PEG-GTPDSRLDW-----GPDMTCSDDTQYSNG--RGH- 162
 Qy 185 KAWDEVDTENGNYDYLMYADIDMDHPEVNNELRWGYYNTLGLDFRIDAVKHYS 244

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Db 163 -----RDTGADGAAPDIDHLNTRVQTELSLWNLKSDVGFDFGWRDLDFAGYSAA 213
Qy 245 FTRDWINHVSATGKNMFAVAEFWKN-----DLGATENYLQKTNWHSVF 289
Db 214 VAKTYVDNTDPS-----FVVAEISWNRVYDNGEPEPSWNQDGRQDELVWNAQAVGGPASAF 268
Qy 290 DVELHNLVYNASKSGGNDYMRNIFNGT---VVQRHPSHAVTFVDNHDSDQPEEALSFVEE 346
Db 269 DFTTKGEL-QAAVQGLWRMKD-GNGKAPGMIGWLPEKAVTFIDNHD-----GSTQNS 320
Qy 347 WFKP-----LAYALTITREGYPSVFGYDYGIPTHGVPAMRSKIDPILBARQYAYGKQ 401
Db 321 WPFPSDKVMQGYAYILT-HPGVPCIFY----- 346
Qy 402 NDYLDHNNIGW-----TREGNTAHPNSGLATIMSDG 433
Db 347 -----DH---VFDWNLKQEIISTLAVRSRNEIHPGSKLKILAREG 383

RESULT 12
AM3D_ORYSA
ID_AM3D_ORYSA STANDARD; PRT; 435 AA.
AC P27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.3 OR AMY3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etisolated leaf;
RX MEDLINE=91088278; PubMed=2263460;
RA Huang N., Koizumi N., Reinl S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
RT amylase genes.";
RL Nucleic Acids Res. 18:7007-7014 (1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
RA Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
RT clones and mRNA expression during seed germination.";
RL Mol. Gen. Genet. 221:235-244 (1990).
CC -!- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Is expressed in all tissues, except in
CC immature seeds. Is the most abundant alpha-amylase isozyme in
CC callus.
CC -!- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurones cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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or send an email to license@isb-sib.ch).
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DR EMBL; M59351; AAA33895.1; -.
DR EMBL; M24287; AAA33886.1; -.
DR PIR; S12625; S12625.
DR HSSP; P04063; 1AVA.
DR Gramene; P27933; -.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amyy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 435
FT ACT_SITE 203 203
FT ACT_SITE 311 311
FT METAL 116 116
FT METAL 133 133
FT METAL 136 136
FT METAL 138 138
FT METAL 141 141
FT METAL 151 151
FT METAL 162 162
FT METAL 167 167
FT METAL 170 170
FT METAL 172 172
FT CONFLICT 73 74
FT CONFLICT 137 137
SQ SEQUENCE 435 AA; 47911 MW; 1BBD6AB195BA0D6E CRC64;

Query Match 9.8%; Score 264.5; DB 1; Length 435;
Best Local Similarity 25.6%; Pred. No. 5.2e-11;
Matches 100; Conservative 50; Mismatches 150; Indels 91; Gaps 19;

Qy 2 HNGTNGTMMQYFEW-YLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
Db 21 NSGQAQVLFGFNWESWKQGGWYNNLKGQVDDIAKAGVTHVWLPSPSHVAPQ--GYMP 78
Qy 61 YDIYDLGEFNQKGTVTYKTSQQAATSLKNGNGIOVGVVMMHKGADATENVRAV 120
Db 79 GRLYDLD-----ASKYGTAAELKSLTAAFHFGKGVQCVADVVIH-----RCA 120
Qy 121 EVNPNRNRQEVTEGYTIEAWTRDFPFGNGNTHSSFKRWYHFDVGDVDSRRLLNRIYKF 180
Db 121 E-----KKDARGVYCV-----PE-----GGTP-----DRLDWGPGMICSDDTQYS 155
Qy 181 RGHGKAWDEVDTEGNYDYLMYADIDMDHPEVNVNELRWGVYVYTLGLDGFRIIDAVKH 240
Db 156 DGTGHR-----DTGEG---FGAAPDIDHLNPRVQRELTDNLNWLKSDVGFDFGWRDLDFAGK 207
Qy 241 IKYSFTFDWINHVSATGKNMFAVAEFWKN-----DLGAIENYLQKTNWHS 287
Db 208 YSTDIAMKYVESCKPG-----FVVAEISWNLKSGGNDYMRNIFNGT---VVQRHPSHAVTFVDNHDSDQPEE 338
Qy 288 V-----FDVPLHNLVYNASKSGGNDYMRNIFNGT---VVQRHPSHAVTFVDNHDSDQPEE 338
Db 259 VGGPAMTFDTTK-GLLQAGVQGLWRDLR-D-GNGKAPGMIGWLPEKAVTFVDNHDGTSIQ 316
Qy 339 ALESP-VEEMFKPLAYALTITREGYPSVFPY 368
Db 317 KLWPFPSDKVMQGYAYILT-HPGVPCIFY 344

RESULT 13
AMT4_PSESA
ID_AMT4_PSESA STANDARD; PRT; 551 AA.
AC P22963;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
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EMBL; K02638; AAA32933.1; --
DR HSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHARAMYLASE.
DR SMART; SMO0642; Amy; 1.
KW Germination; Carbohydrate metabolism; Hydrolase; Glycosidase; Seed;
KW Calcium-binding; Signal; Multigene family.
FT SIGNAL 1 24
FT CHAIN 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 228 228 BY SIMILARITY.
FT ACT_SITE 313 313 BY SIMILARITY.
FT METAL 115 115 CALCIUM 1 (BY SIMILARITY).
FT METAL 132 132 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 137 137 CALCIUM 2 (BY SIMILARITY).
FT METAL 141 141 CALCIUM 2 (BY SIMILARITY).
FT METAL 151 151 CALCIUM 3 (BY SIMILARITY).
FT METAL 162 162 CALCIUM 3 (VIA CARBONYL OXYGEN).
FT METAL 165 165 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
FT METAL 166 166 CALCIUM 1 (BY SIMILARITY).
FT METAL 167 167 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
FT METAL 170 170 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
FT METAL 172 172 CALCIUM 1 AND 3 (BY SIMILARITY).
FT NON_TER 368 368
SQ SEQUENCE 368 AA; 40787 MW; A237EF55793BA93B CRC64;

Query Match 9.6%; Score 260; DB 1; Length 368;
Best Local Similarity 24.3%; Pred. No. 8.6e-11;
Matches 101; Conservative 59; Mismatches 148; Indels 108; Gaps 18;

Qy 9 MMQYFEH-YLPDNGHNHRLNSDASNLKSGITAVIWPAPKASQNDVGYDYLGLG 67
Db 27 LFQGFNWSKNGGWTFNLMGKYDDIAAAGITHVWLPASQSVAEQ--GYMFGRLYDLD 84
Qy 68 EFNQKGVTRTKYTRSQLOAAVTSLNKNGIQVYGVDMVHKGADATEMVRVAVNPNNR 127
Db 85 -----ASKYGNKAQLKSLIGHGKGVKATADIVNHR----- 117
Qy 128 NQEVGTYYTTEAWTRDFPGRGNTHSSFKRWYHFDGV-----DWDQSRLLANNRYKFR 181
Db 118 -----TAEHK-----DGRG-----IYCFEGVTPDRLDWMGHMCRDRPYAD 156
Qy 182 GHGKAWDEVDTENGNYDLYMADI DMHPFVNVNLRNNGWYNTVLTGLDPRIDAVKHI 241
Db 157 GTGNP-----DT-----GADFGAAPDIDLNLRVQKELAEWLNWKADTGFDGWRPFAKY 208
Qy 242 KYSTPRDWINHVRSATCKNMFVAFAEFW-----KNDLGATENYLOKTNWHSV----- 288
Db 209 SADVAKIYDR-----SEPSFAVAEITWISLAYGDDGPNLNQDHRQELVNWVDKVGKG 263
Qy 289 -----FDVPLHYNLNASKSGNYDMRNI FNGT-----VVQRHPSHATVTFVDNHSOPEE 338
Db 264 PATTFDFTTK-GILNVAVEGBELWLR-----GTDGKAPGMIGWMPAKAVTFVDNHDGTSTQ 318
Qy 339 ALESF-VVEWFKPLAYALTLTREOGYPSVFVDYGIPTGCVPMRSKIDPILLEAR 393
Db 319 HMWPFPSDRVMQVAYIILT---HPGTPCIFYDHFDDW-----GLKEIDRLVSVR 365

RESULT 15

AMT4_PSEST STANDARD; PRT; 548 AA.
AC FI3507;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-
DE amylase) (Maltotetraose-forming amylase) (Exo-maltotetraohydrolase)
DE (Maltotetraose-forming exo-amylase).
GN AMYP.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=MO-19;
RX MEDLINE=89155431; PubMed=2646279;
RA Fujita M., Torigoe K., Nakada T., Tsusaki K., Kubota M., Sakai S.,
RA Tsujisaka Y.;
RT "Cloning and nucleotide sequence of the gene (amyP) for
RT maltotetraose-forming amylase from Pseudomonas stutzeri MO-19.";
RL J. Bacteriol. 171:1333-1339(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 286-302.
RC STRAIN=MO-19;
RX MEDLINE=97271999; PubMed=9126844;
RA Morishita Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.,
RA Sakai S.;
RT "Crystal structure of a maltotetraose-forming exo-amylase from
RT Pseudomonas stutzeri.";
RL J. Mol. Biol. 267:661-672(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF VARIANT GLN-240.
RC STRAIN=MO-19;
RX MEDLINE=97428332; PubMed=9281429;
RA Yoshioka Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.;
RT "Crystal structures of a mutant maltotetraose-forming exo-amylase
RT cocrySTALLIZED with maltopentaose.";
RL J. Mol. Biol. 271:619-628(1997).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF VARIANTS.
RC STRAIN=MO-19;
RX MEDLINE=20027472; PubMed=10556241;
RA Hasegawa K., Kubota M., Matsuura Y.;
RT "Roles of catalytic residues in alpha-amylases as evidenced by the
RT structures of the product-complexed mutants of a maltotetraose-forming
RT amylase.";
RL Protein Eng. 12:819-824(1999).
CC -I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
CC in amylaceous polysaccharides so as to remove successive
CC maltotetraose residues from the non-reducing chain ends.
CC -I- COFACTOR: Binds 2 calcium ions per subunit.
CC -I- PATHWAY: Starch degradation.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- MISCELLANEOUS: THERE ARE SEVERAL ISOENZYME FORMS OF THIS PROTEIN.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M24516; AAA25707.1; --
DR PUR; A32803; A32803.
DR PDB; 1GCY; 28-JAN-03.

DR PDB; 1JDA; 15-OCT-97.
 DR PDB; 1JDC; 15-OCT-97.
 DR PDB; 1JDD; 15-OCT-97.
 DR PDB; 1Q13; 24-NOV-99.
 DR PDB; 1Q14; 24-NOV-99.
 DR PDB; 1Q15; 24-NOV-99.
 DR PDB; 1QPK; 17-NOV-99.
 DR PDB; 2AMG; 01-APR-97.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 548
 FT ACT_SITE 214 214
 FT ACT_SITE 240 240
 FT ACT_SITE 315 315
 FT METAL 22 22
 FT METAL 23 23
 FT METAL 34 34
 FT METAL 37 37
 FT METAL 38 38
 FT METAL 137 137
 FT METAL 172 172
 FT METAL 175 175
 FT METAL 183 183
 FT METAL 218 218
 FT DISULFID 161 171
 FT DISULFID 237 272
 FT CONFLICT 286 302
 FT TURN 28 29
 FT TURN 34 35
 FT STRAND 40 42
 FT TURN 46 47
 FT HELIX 48 51
 FT TURN 53 55
 FT HELIX 56 62
 FT TURN 63 63
 FT HELIX 64 69
 FT TURN 70 71
 FT STRAND 74 77
 FT STRAND 87 89
 FT TURN 90 91
 FT STRAND 92 94
 FT TURN 99 100
 FT STRAND 108 108
 FT TURN 109 110
 FT STRAND 111 111
 FT HELIX 113 126
 FT TURN 127 127
 FT STRAND 129 134
 FT STRAND 138 138
 FT TURN 141 142
 FT TURN 152 153
 FT STRAND 157 157
 FT HELIX 158 160
 FT STRAND 169 169
 FT TURN 170 171
 FT STRAND 172 172
 FT TURN 178 179
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 FT TURN 186 187
 FT HELIX 189 205
 FT STRAND 208 213
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 FT HELIX 221 231

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 CALCIUM 2.
 CALCIUM 2 (VIA CARBONYL OXYGEN).
 CALCIUM 2.
 CALCIUM 2.
 CALCIUM 2.
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 CALCIUM 1.
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 FT STRAND 403 408
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 SQ SEQUENCE 548 AA; 59876 MW; 2B87217B3379158F CRC64;

Query Match 9.6%; Score 259; DB 1; Length 548;
 Best Local Similarity 23.6%; Pred. No. 1.6e-10;
 Matches 124; Conservative 68; Mismatches 168; Indels 166; Gaps 26;

QY 2 HNGTNGTMMQVFEWYL----PNDGNHNRNLSNLSKSGITAVWIPPAWKASQNDVG 57
 DB 33 YHGGDEILQGFHWNVREAPND--WYNLRQQAATTAADGFSAINWPFVWRDFSSWSDG 90
 QY 58 --YGAYDLYDLGEFNGKGTVRTKYGTRSQLQAAVTSLNKNGIQVYGVVMNH--KGGADA 113
 DB 91 SKSGGGEYFWDHFNKNG---RYGSDAQLRQAASALGGAGVKLYDVPVHNRGYPDK 146
 QY 114 TEMVRAVEVN--PNNRNOEVTGEYTIETAWTRDFPGRGNTHSSFKRWYHDFGVNDQSR 172
 DB 147 -----EINLPAG-----QGFWRNDCADPGN-----YPNDCDDGD--- 175
 QY 173 LNNRIYKFRGHKAWDWEVDTENGNYDLYMAYADIDMDHPVNVNLRNNGVYNTLGLDG 232
 DB 176 -----RFIG-----ADLNTGHPQVYGMFRDEFNLRQYAGG 210
 QY 233 FRIDAVKHIKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAIE---NYLQKTNNH-- 286
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 QY 287 -----SVFDVPLHYNLYNASKSGNVDNRNIFNGTVVQRHPSHAVTFVDNHDQPE 337
 DB 264 KDWSDRAKCPVDFDFALKERMQNGSIA---DWKHGLNGNDPDRWREVAVTVDNHDGTYS 319
 QY 338 BALESFVEW-----FKPLAYALTIREQYPSVF-----YGDYVYGIPTHCVPNRS 384
 DB 320 PGQNGGQHHLALQGLIRQAYILT-SPGTVPVYSHMYDWDGYGDP----- 365
 QY 385 KIDPILFARQKAYGKQNDYLDHNNIIGWTRREGNTAHPNSGLATIMSDGAGGKWMFVGR 444
 DB 366 -IRQLIQVR--AAG-----VRASATSFHSGYGLVATVSGSQQTLLVAL 408
 QY 445 N-----KAGQVWSDTGNRTCTVTINADGWGNFS-----VNGGVSIV 482
 DB 409 NSDLGNPGQVAS-----GSFSEAVNASNGQVRVW 437

us-09-925-576c-13.rsp

Thu Oct 7 08:31:55 2004

Search completed: October 7, 2004, 00:13:27
Job time : 10.5063 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 15.0278 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-13
Perfect score: 2703
Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGKNFVNGSGSVSIWVK 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	485	3	US-08-600-656-7
2	2703	100.0	485	3	US-09-170-670-6
3	2703	100.0	485	3	US-09-193-068-6
4	2703	100.0	485	3	US-09-183-412-6
5	2703	100.0	485	3	US-09-354-191A-7
6	2703	100.0	485	4	US-09-291-023A-13
7	2703	100.0	485	4	US-09-290-734-6
8	2703	100.0	485	4	US-09-381-687-5
9	2703	100.0	485	4	US-09-545-586-6
10	2703	100.0	485	4	US-09-540-715A-13
11	2703	100.0	485	4	US-09-769-864-6
12	2613	96.7	485	4	US-09-290-734-24
13	2613	96.7	485	4	US-09-230-734-26
14	2613	96.7	485	4	US-09-417-359A-5
15	2613	96.7	485	4	US-09-545-586-24
16	2613	96.7	485	4	US-09-545-586-26
17	2440	90.3	485	2	US-08-446-803-1
18	2440	90.3	485	2	US-08-861-837-1
19	2440	90.3	485	2	US-08-600-308A-12
20	2440	90.3	485	3	US-08-683-838A-12
21	2440	90.3	485	3	US-08-600-656-1
22	2440	90.3	485	3	US-09-170-670-1
23	2440	90.3	485	3	US-09-170-670-7
24	2440	90.3	485	3	US-09-193-068-1
25	2440	90.3	485	3	US-09-193-068-7
26	2440	90.3	485	3	US-09-183-412-1
27	2440	90.3	485	3	US-09-183-412-7

28	2440	90.3	485	3	US-09-354-191A-1	Sequence 1, Appli
29	2440	90.3	485	4	US-09-291-023A-19	Sequence 19, Appli
30	2440	90.3	485	4	US-09-290-734-1	Sequence 1, Appli
31	2440	90.3	485	4	US-09-290-734-7	Sequence 7, Appli
32	2440	90.3	485	4	US-09-636-252A-12	Sequence 12, Appli
33	2440	90.3	485	4	US-09-381-687-2	Sequence 2, Appli
34	2440	90.3	485	4	US-09-545-586-1	Sequence 7, Appli
35	2440	90.3	485	4	US-09-545-586-7	Sequence 19, Appli
36	2440	90.3	485	4	US-09-540-715A-19	Sequence 1, Appli
37	2440	90.3	485	4	US-09-769-864-1	Sequence 7, Appli
38	2440	90.3	485	4	US-09-769-864-7	Sequence 7, Appli
39	2436	90.1	485	3	US-09-284-097-7	Sequence 4, Appli
40	2425.5	89.7	486	4	US-09-381-687-4	Sequence 7, Appli
41	2414	89.3	485	2	US-08-446-803-2	Sequence 2, Appli
42	2414	89.3	485	2	US-08-861-837-2	Sequence 2, Appli
43	2414	89.3	485	3	US-08-600-656-2	Sequence 2, Appli
44	2414	89.3	485	3	US-09-170-670-2	Sequence 2, Appli
45	2414	89.3	485	3	US-09-170-670-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-600-656-7
; Sequence 7, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6093562o No. 6093562disk of No. 6093562th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,656
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-600-656-7

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGASQNDVGGA 60
Db 1 HHNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGASQNDVGGA 60

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DB 61 YDLYLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
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QY 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNVNELRNWGWYNTTILGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNVNELRNWGWYNTTILGLDGFRI DAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLQKTNWNHSDVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLQKTNWNHSDVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRNI FNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNI FNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSPFYGDYIGIPHTGVPAMRSKIDPILBARQYAYGKONDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSPFYGDYIGIPHTGVPAMRSKIDPILBARQYAYGKONDYLDHNNIIGWTRGNTA 420
QY 421 HPNSGLATIMSDGAGGSKWMFVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKWMFVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 2
US-09-170-670-6
; Sequence 6, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-6

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
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DB 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNVNELRNWGWYNTTILGLDGFRI DAVKH 240
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DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLQKTNWNHSDVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRNI FNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNI FNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE 360
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QY 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNVNELRNWGWYNTTILGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNVNELRNWGWYNTTILGLDGFRI DAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLQKTNWNHSDVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLQKTNWNHSDVDPVPLHYNLYNA 300
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DB 301 SKSGGNYDMRNI FNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE 360
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DB 361 QGYPSPFYGDYIGIPHTGVPAMRSKIDPILBARQYAYGKONDYLDHNNIIGWTRGNTA 420
QY 421 HPNSGLATIMSDGAGGSKWMFVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKWMFVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 3
US-09-193-068-6
; Sequence 6, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjulliff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-6

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
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QY 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNVNELRNWGWYNTTILGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNVNELRNWGWYNTTILGLDGFRI DAVKH 240
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QY 301 SKSGGNYDMRNI FNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE 360
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DB 361 QGYSVFYDGYGIPTHGVPMRKSIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
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DB 481 IWVWK 485

RESULT 4

US-09-183-412-6
; Sequence 6, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-6

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 HNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
QY 61 YDLGLGEFQKGTVRTKGYTRSQLQAATVSLKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLGLGEFQKGTVRTKGYTRSQLQAATVSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNEQVTEGTYTEAWTRFDPGRGNTHSSFKRWYHFDGVDQSRLLNNRIYKF 180
DB 121 EVNPNRNEQVTEGTYTEAWTRFDPGRGNTHSSFKRWYHFDGVDQSRLLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNYDYLMDYADIMDHPVNVNLRNMGVWYTNLTGLDGFRIADVX 240
DB 181 RGHGKAWDEVDTEGNYDYLMDYADIMDHPVNVNLRNMGVWYTNLTGLDGFRIADVX 240
QY 241 IKYSFTRDWINHRSATGKNFAVAEFKNDLGAENYLOKTNWHSVDFVPLHNLNYNA 300
DB 241 IKYSFTRDWINHRSATGKNFAVAEFKNDLGAENYLOKTNWHSVDFVPLHNLNYNA 300
QY 301 SKSGGNYDMENIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTRE 360
DB 301 SKSGGNYDMENIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTRE 360

QY 361 QGYSVFYDGYGIPTHGVPMRKSIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYSVFYDGYGIPTHGVPMRKSIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 5

US-09-354-191A-7
; Sequence 7, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-354-191A-7

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
DB 1 HNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
QY 61 YDLGLGEFQKGTVRTKGYTRSQLQAATVSLKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLGLGEFQKGTVRTKGYTRSQLQAATVSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNEQVTEGTYTEAWTRFDPGRGNTHSSFKRWYHFDGVDQSRLLNNRIYKF 180
DB 121 EVNPNRNEQVTEGTYTEAWTRFDPGRGNTHSSFKRWYHFDGVDQSRLLNNRIYKF 180

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QY 181 RHGKAWDEVDTEGNYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVDFPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVDFPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HNSGLATIMSDGAGGSKMFMVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
DB 421 HNSGLATIMSDGAGGSKMFMVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 6
US-09-291-023A-13
; Sequence 13, Application US/09291023A
; Patent No. 6309871
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Activity And Nucleic
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291.023A
; PRIOR FILING DATE: 1999-04-13
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-13

Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223; Indels 0; Gaps 0;
Matches 485; Conservative 0; Mismatches 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLVDLGEFNGKQGTVRTKTYGTRSQLQAAVTSLKNGIQYGVGVMMHKGADATEMVRV 120
DB 61 YDLVDLGEFNGKQGTVRTKTYGTRSQLQAAVTSLKNGIQYGVGVMMHKGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNRQEVGTGYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
QY 181 RHGKAWDEVDTEGNYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVDFPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVDFPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
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DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVDFPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HNSGLATIMSDGAGGSKMFMVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
DB 421 HNSGLATIMSDGAGGSKMFMVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 7
US-09-290-734-6
; Sequence 6, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989-1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290.734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-6

Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223; Indels 0; Gaps 0;
Matches 485; Conservative 0; Mismatches 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLVDLGEFNGKQGTVRTKTYGTRSQLQAAVTSLKNGIQYGVGVMMHKGADATEMVRV 120
DB 61 YDLVDLGEFNGKQGTVRTKTYGTRSQLQAAVTSLKNGIQYGVGVMMHKGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNRQEVGTGYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
QY 181 RHGKAWDEVDTEGNYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVDFPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVDFPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
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Db 361 QGYPVFGYDYGIPHTGVPAWRSKIDPILAEARQKAYAKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 8
US-09-381-687-5
; Sequence 5, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-011SP
; CURRENT APPLICATION NUMBER: US/09/381.687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp. #707
US-09-381-687-5

Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Qy 61 YDYLDELGEFQKQVTRTKYGRSOLQAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDYLDELGEFQKQVTRTKYGRSOLQAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVTEYTTIEAWTRDFPGRGNTSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVTEYTTIEAWTRDFPGRGNTSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
Qy 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPVFGYDYGIPHTGVPAWRSKIDPILAEARQKAYAKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVFGYDYGIPHTGVPAWRSKIDPILAEARQKAYAKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 10
US-09-540-715A-13
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Db 481 IWVWK 485

RESULT 9
US-09-545-586-6
; Sequence 6, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545.586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290.734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-6

Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Qy 61 YDYLDELGEFQKQVTRTKYGRSOLQAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDYLDELGEFQKQVTRTKYGRSOLQAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVTEYTTIEAWTRDFPGRGNTSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVTEYTTIEAWTRDFPGRGNTSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
Qy 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPVFGYDYGIPHTGVPAWRSKIDPILAEARQKAYAKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVFGYDYGIPHTGVPAWRSKIDPILAEARQKAYAKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 10
US-09-540-715A-13
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; Sequence 13, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Acid
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
; US-09-540-715A-13

Query Match      100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGASQNDVGYGA 60
QY 61 YDLYLGEFNQKGTVRTKYGTRSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYLGEFNQKGTVRTKYGTRSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQEVGTGEYITIAWTRFDPGNGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVGTGEYITIAWTRFDPGNGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEWDTENGNDYLMYADIMDHPVNVNELRNWGVYNTLTGLDGRIDAVKH 240
Db 181 RGHGKAWDEWDTENGNDYLMYADIMDHPVNVNELRNWGVYNTLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300
QY 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTIRE 360
Db 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTIRE 360
QY 361 QGYPSVFYGYDYGIPTHGVPMRSKIDPILAEARQKYAYKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPMRSKIDPILAEARQKYAYKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMVFGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMVFGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 11
US-09-769-864-6
; Sequence 6, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne

; Sequence 13, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Acid
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-09-769-864-6

Query Match      100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGASQNDVGYGA 60
QY 61 YDLYLGEFNQKGTVRTKYGTRSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYLGEFNQKGTVRTKYGTRSQLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQEVGTGEYITIAWTRFDPGNGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVGTGEYITIAWTRFDPGNGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEWDTENGNDYLMYADIMDHPVNVNELRNWGVYNTLTGLDGRIDAVKH 240
Db 181 RGHGKAWDEWDTENGNDYLMYADIMDHPVNVNELRNWGVYNTLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300
QY 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTIRE 360
Db 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTIRE 360
QY 361 QGYPSVFYGYDYGIPTHGVPMRSKIDPILAEARQKYAYKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPMRSKIDPILAEARQKYAYKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMVFGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMVFGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 12
US-09-290-734-24
; Sequence 24, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Prantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-24

Query Match
Best Local Similarity 96.7%; Score 2613; DB 4; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVTIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGISAVTIPPAWKASQNDVGYGA 60

Qy 61 YDLVLDGEFNQKGTIRTKYGRSOLQAQAVTSLKNGIQVYGDVVVNNHKGADATEMVRV 120
Db 61 YDLVLDGEFNQKGTIRTKYGRNQLQAQAVNALKNGIQVYGDVVVNNHKGADATEMVRV 120

Qy 121 EVNPNRNQEVGTGEYTTIEATRFDPGGRNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEATWKFDPPGGRNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180

Qy 181 RGHGKANDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240

Qy 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLNKTNWNHVSFVDFVPLHYNLYNA 300

Qy 301 SKSGNCDMRNIFNGTVVQRHPSHAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360
Db 301 SKSGNCDMRQIFNGTVVQRHPMEAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360

Qy 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILKARQYAGKONDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILKARQYAGKONDYLDHNNIIGWTREGNTA 420

Qy 421 HPNSGLATIMSDGAGGSKMFPVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFPVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 13
US-09-290-734-26
; Sequence 26, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-26

Query Match
Best Local Similarity 96.7%; Score 2613; DB 4; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVTIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGISAVTIPPAWKASQNDVGYGA 60

Qy 61 YDLVLDGEFNQKGTIRTKYGRSOLQAQAVTSLKNGIQVYGDVVVNNHKGADATEMVRV 120
Db 61 YDLVLDGEFNQKGTIRTKYGRNQLQAQAVNALKNGIQVYGDVVVNNHKGADATEMVRV 120

Qy 121 EVNPNRNQEVGTGEYTTIEATRFDPGGRNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEATWKFDPPGGRNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180

Qy 181 RGHGKANDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240

Qy 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLNKTNWNHVSFVDFVPLHYNLYNA 300

Qy 301 SKSGNCDMRNIFNGTVVQRHPSHAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360
Db 301 SKSGNCDMRQIFNGTVVQRHPMEAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360

Qy 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILKARQYAGKONDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILKARQYAGKONDYLDHNNIIGWTREGNTA 420

Qy 421 HPNSGLATIMSDGAGGSKMFPVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFPVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 IWVWK 485
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RESULT 14
US-09-417-359A-5
; Sequence 5, Application US/09417359A
; Patent No. 6461849
; GENERAL INFORMATION:
; APPLICANT: Oleen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/09/417,359A
; CURRENT FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-417-359A-5

Query Match
Best Local Similarity 96.7%; Score 2613; DB 4; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
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Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;	
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Db	1 HNGTGTGTMQYFEWYLPNDGNHNRNLNSDASNLKSGISAVWIPPAWKGASQNDVGGA 60
Qy	61 YDLYDLGFEFNQGTVRTKYGTRSQQAQAVTSLKNGGIQVYGDVVMNHKGGADATEMVRV 120
Db	61 YDLYDLGFEFNQGTVRTKYGTRNQQAQAVNALKSGIQVYGDVVMNHKGGADATEMVRV 120
Qy	121 EVNPNRNRQEVTCYTIETAWTRFDPPGRGNTHSSFKRWYHFDGVDWDQSRRLNRIYKF 180
Db	121 EVNPNRNRQEVSGEYTIETAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Qy	181 RHGKAWDEVDTEGNGNDYLYMYADIDMDHPEVNVNELRWGWYNTNLGLDGFRIIDAVKH 240
Db	181 RHGKAWDEVDTEGNGNDYLYMYADIDMDHPEVNVNELRWGWYNTNLGLDGFRIIDAVKH 240
Qy	241 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLKTNWNHVSFVDPVPLHYNLYNA 300
Db	241 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLKTNWNHVSFVDPVPLHYNLYNA 300
Qy	301 SKSGGNYDMRNIIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
Db	301 SKSGGNYDMRQIFNGTVVQRHPHMAVTFVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
Qy	361 QGYPSVFGDYGIPTGHPVPAMRSKIDPILARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
Db	361 QGYPSVFGDYGIPTGHPVPAMRSKIDPILARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
Qy	421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
Db	421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGVS 480
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Db	481 IWVWK 485

RESULT 15

US-09-545-586-24
; Sequence 24, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545,586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-24

Query Match 96.7%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 2.3e-215;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
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Db 1 HNGTGTGTMQYFEWYLPNDGNHNRNLNSDASNLKSGISAVWIPPAWKGASQNDVGGA 60

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Db	61 YDLYDLGFEFNQGTVRTKYGTRNQQAQAVNALKSGIQVYGDVVMNHKGGADATEMVRV 120
Qy	121 EVNPNRNRQEVTCYTIETAWTRFDPPGRGNTHSSFKRWYHFDGVDWDQSRRLNRIYKF 180
Db	121 EVNPNRNRQEVSGEYTIETAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Qy	181 RHGKAWDEVDTEGNGNDYLYMYADIDMDHPEVNVNELRWGWYNTNLGLDGFRIIDAVKH 240
Db	181 RHGKAWDEVDTEGNGNDYLYMYADIDMDHPEVNVNELRWGWYNTNLGLDGFRIIDAVKH 240
Qy	241 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLKTNWNHVSFVDPVPLHYNLYNA 300
Db	241 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLKTNWNHVSFVDPVPLHYNLYNA 300
Qy	301 SKSGGNYDMRNIIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
Db	301 SKSGGNYDMRQIFNGTVVQRHPHMAVTFVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
Qy	361 QGYPSVFGDYGIPTGHPVPAMRSKIDPILARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
Db	361 QGYPSVFGDYGIPTGHPVPAMRSKIDPILARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
Qy	421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
Db	421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGVS 480
Qy	481 IWVWK 485
Db	481 IWVWK 485

Search completed: October 7, 2004, 00:47:14
Job time : 16.0278 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-13

Perfect score: 2703

Sequence: 1 HHNGTGTMMQYFEWLPND.....ADGNGFVNGSGSVIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2703	100.0	485	9	US-09-854-346-13
3	2703	100.0	485	9	US-09-902-188A-7
4	2703	100.0	485	10	US-09-925-576C-13
5	2703	100.0	485	12	US-10-665-667-6
6	2703	100.0	485	12	US-10-025-648-7
7	2703	100.0	485	12	US-10-327-837-6
8	2703	100.0	485	16	US-10-477-725-13
9	2613	96.7	485	9	US-09-854-346-12
10	2613	96.7	485	9	US-09-918-543-12
11	2613	96.7	485	10	US-09-925-576C-12
12	2613	96.7	485	12	US-10-327-837-24
13	2613	96.7	485	12	US-10-327-837-26
14	2613	96.7	485	14	US-10-209-812-5
15	2613	96.7	485	16	US-10-477-725-12

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17	2440	90.3	485	9	US-09-769-864-1	Sequence 1, Appli
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19	2440	90.3	485	9	US-09-854-346-2	Sequence 2, Appli
20	2440	90.3	485	9	US-09-902-188A-1	Sequence 1, Appli
21	2440	90.3	485	9	US-09-918-543-2	Sequence 2, Appli
22	2440	90.3	485	9	US-09-795-211-1	Sequence 1, Appli
23	2440	90.3	485	10	US-09-925-576C-2	Sequence 2, Appli
24	2440	90.3	485	12	US-10-665-667-1	Sequence 1, Appli
25	2440	90.3	485	12	US-10-665-667-7	Sequence 7, Appli
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29	2440	90.3	485	14	US-10-184-771-12	Sequence 12, Appli
30	2440	90.3	485	16	US-10-477-725-2	Sequence 2, Appli
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33	2414	89.3	485	9	US-09-854-346-4	Sequence 4, Appli
34	2414	89.3	485	9	US-09-902-188A-2	Sequence 2, Appli
35	2414	89.3	485	9	US-09-918-543-4	Sequence 4, Appli
36	2414	89.3	485	9	US-09-795-211-2	Sequence 2, Appli
37	2414	89.3	485	10	US-09-925-576C-4	Sequence 4, Appli
38	2414	89.3	485	12	US-10-665-667-2	Sequence 2, Appli
39	2414	89.3	485	12	US-10-665-667-8	Sequence 8, Appli
40	2414	89.3	485	12	US-10-025-648-2	Sequence 2, Appli
41	2414	89.3	485	12	US-10-327-837-2	Sequence 2, Appli
42	2414	89.3	485	12	US-10-327-837-8	Sequence 8, Appli
43	2414	89.3	485	16	US-10-477-725-4	Sequence 4, Appli
44	2410	89.2	516	9	US-09-986-676A-2	Sequence 2, Appli
45	2410	89.2	516	9	US-09-971-611-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-769-864-6
; Sequence 6, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-6

Query Match 100.0%; Score 2703; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	YDLYDLGEFNQKGTVRTKYSQLOAAVTSLKNGIQVYGVVNMHKGADATEMVRV	120
QY	121	EVNPNRNEQVTEYTIETATWTRDFPGRGNTHSSFKRWVHFDGVDWDQSRLLNNRIYKF	180

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Qy 181 RGHGKAWDEVDTENGNDYLYMAYADIDMDHPPEVNNELRWGVYNTNLTGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTENGNDYLYMAYADIDMDHPPEVNNELRWGVYNTNLTGLDGFRIIDAVKH 240
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Db 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE 360
Qy 361 QGYPSVFYGDYIGIPTHGVPAMRSKIDPILBARQKAYGKQNDYLDHNNIIGWTRREGNTA 420
Db 361 QGYPSVFYGDYIGIPTHGVPAMRSKIDPILBARQKAYGKQNDYLDHNNIIGWTRREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Db 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
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RESULT 2
US-09-854-346-13
; Sequence 13, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus 707
US-09-854-346-13

Query Match 100.0%; Score 2703; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGKITAVWIPPAWKASQNDVGYGA 60
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Qy 61 YDLYDLGEFNGKGTVRTKYGTRSQLQAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
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Qy 121 EVNPNRNQEVITGEYTIETATRFDPFGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
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Qy 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE 360
Db 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE 360
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Qy 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Db 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Qy 481 IWVNK 485
Db 481 IWVNK 485

RESULT 3
US-09-902-188A-7
; Sequence 7, Application US/09902188A
; Patent No. US20020098996A1
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; Svendsen, Allan
; Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. US20020098996A1o No. US20020098996A1disk of No. US20020098996A1
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/902,188A
; FILING DATE: 10-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/354,191
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-902-188A-7

Query Match 100.0%; Score 2703; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 YDLYDLGEFNQKGVTRTKYGRSLOQAQVTSKNGGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVTEYTTIEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVTEYTTIEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNGVWYNTLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNGVWYNTLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWLNHRSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWLNHRSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGNDYMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNDYMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYDYGIGIPTHGVPAMRSKIDPILFARQYAYKQNDYLDHNNIIGWTRGNNTA 420
Db 361 QGYPSVFYDYGIGIPTHGVPAMRSKIDPILFARQYAYKQNDYLDHNNIIGWTRGNNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 4

US-09-925-576C-13
; Sequence 13, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: bacillus sp. 707
US-09-925-576C-13

Query Match 100.0%; Score 2703; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNQKGVTRTKYGRSLOQAQVTSKNGGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNQKGVTRTKYGRSLOQAQVTSKNGGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVTEYTTIEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVTEYTTIEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNGVWYNTLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNGVWYNTLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWLNHRSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300

Db 241 IKYSFTRDWLNHRSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGNDYMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNDYMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYDYGIGIPTHGVPAMRSKIDPILFARQYAYKQNDYLDHNNIIGWTRGNNTA 420
Db 361 QGYPSVFYDYGIGIPTHGVPAMRSKIDPILFARQYAYKQNDYLDHNNIIGWTRGNNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 5

US-10-665-667-6
; Sequence 6, Application US/10665667
; Publication No. US20040039368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; PRIOR FILING DATE: 2003-09-19
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-6

Query Match 100.0%; Score 2703; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNQKGVTRTKYGRSLOQAQVTSKNGGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNQKGVTRTKYGRSLOQAQVTSKNGGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVTEYTTIEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVTEYTTIEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNGVWYNTLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNGVWYNTLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWLNHRSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWLNHRSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGNDYMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNDYMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360

Qy	361	QGYPSVFYGDYYGITHGVPMR	SKIDPIL	EARQK	YAGK	ONDYLDH	HNII	GW	TREGNTA	420
Db	361	QGYPSVFYGDYYGITHGVPMR	SKIDPIL	EARQK	YAGK	ONDYLDH	HNII	GW	TREGNTA	420
Qy	421	HPNSGLATIMSDGAGSKWMF	VGVRNKA	QGVNSDIT	GNRTG	FTVTINAD	GWGNF	SVNGGS	VS	480
Db	421	HPNSGLATIMSDGAGSKWMF	VGVRNKA	QGVNSDIT	GNRTG	FTVTINAD	GWGNF	SVNGGS	VS	480
Qy	481	IWNK	485							
Db	481	IWNK	485							
		RESULT 6								
		US-10-025-648-7								
		; Sequence 7, Application US/10025648								
		; Publication No. US20030064908A1								
		; GENERAL INFORMATION:								
		; APPLICANT: Bisgard-Frantzen, Henrik								
		; Svendsen, Allan								
		; Borchert, Torben Vedel								
		; TITLE OF INVENTION: AMYLASE VARIANTS								
		; NUMBER OF SEQUENCES: 32								
		; CORRESPONDENCE ADDRESS:								
		; ADDRESSEE: Novo Nordisk of North America, Inc.								
		; STREET: 405 Lexington Avenue, Suite 6400								
		; CITY: New York								
		; STATE: New York								
		; COUNTRY: U.S.A.								
		; ZIP: 10174-6401								
		; COMPUTER READABLE FORM:								
		; MEDIUM TYPE: Floppy disk								
		; COMPUTER: IBM PC compatible								
		; OPERATING SYSTEM: PC-DOS/MS-DOS								
		; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)								
		; CURRENT APPLICATION DATA:								
		; APPLICATION NUMBER: US/10/025,648								
		; FILING DATE: 19-Dec-2001								
		; CLASSIFICATION: <Unknown>								
		; PRIOR APPLICATION DATA:								
		; APPLICATION NUMBER: 08/600,656								
		; FILING DATE: 13-FEB-1996								
		; ATTORNEY/AGENT INFORMATION:								
		; NAME: Lambiris, Elias J.								
		; REGISTRATION NUMBER: 33,728								
		; REFERENCE/DOCKET NUMBER: 4318.204-US								
		; TELECOMMUNICATION INFORMATION:								
		; TELEPHONE: 212 867 0123								
		; TELEFAX: 212 867 0298								
		; INFORMATION FOR SEQ ID NO: 7:								
		; SEQUENCE CHARACTERISTICS:								
		; LENGTH: 485 amino acids								
		; TYPE: amino acid								
		; STRANDEDNESS: single								
		; TOPOLOGY: linear								
		; MOLECULE TYPE: peptide								
		; SEQUENCE DESCRIPTION: SEQ ID NO: 7:								
		; US-10-025-648-7								

Db	121	EVAPNNRNQEV	TGEYTTIEAWTRFDPPGRGNTHSSFKWRWYHFDGVDWDQSRRLNNRIYKF	180
Qy	181	RGHGKAWDEW	DTENGNDYILMYADIIMDHPVNVNLRNWGVWYTNLTGLDGFRIIDAVKH	240
Db	181	RGHGKAWDEW	DTENGNDYILMYADIIMDHPVNVNLRNWGVWYTNLTGLDGFRIIDAVKH	240
Qy	241	IKYSFTRDWINHVR	SATGKNMFAVAEFWKNDLGAENYLQKTNNHNSVDFVPLHYNLNA	300
Db	241	IKYSFTRDWINHVR	SATGKNMFAVAEFWKNDLGAENYLQKTNNHNSVDFVPLHYNLNA	300
Qy	301	SKSGNGYDMRNI	FNGTVVQRHPSHAVTFVDNHDSPBEALSFVEEWPKPLAYALTLTRE	360
Db	301	SKSGNGYDMRNI	FNGTVVQRHPSHAVTFVDNHDSPBEALSFVEEWPKPLAYALTLTRE	360
Qy	361	QGVPSVFGDYGI	PTHGVPAMRSKIDPILFARQKIAYGKQNDYLDHNNIIGWTREGNTA	420
Db	361	QGVPSVFGDYGI	PTHGVPAMRSKIDPILFARQKIAYGKQNDYLDHNNIIGWTREGNTA	420
Qy	421	HPNSGLATIMSD	GAGGSKWMPVGNKAGQVMSDITGNRTGTVTINADGWNFSVNGGVS	480
Db	421	HPNSGLATIMSD	GAGGSKWMPVGNKAGQVMSDITGNRTGTVTINADGWNFSVNGGVS	480
Qy	481	IWNK	485	
Db	481	IWNK	485	
RESULT 7				
US-10-327-837-6				
; Sequence 6, Application US/10327837				
; Publication No. US20030211958A1				
; GENERAL INFORMATION:				
; APPLICANT: Svendsen, Allan				
; APPLICANT: Borchert, Torben Vedel				
; APPLICANT: Bisgaard-Frantzen Henrik				
; APPLICANT: Outtrup, Helle				
; APPLICANT: Nielsen, Bjarne Ronfeldt				
; APPLICANT: Nielsen, Vibeke Skovgaard				
; APPLICANT: Hoeck, Lisbeth Hedegaard				
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants				
; FILE REFERENCE: 5276.400-US				
; CURRENT APPLICATION NUMBER: US/10/327,837				
; CURRENT FILING DATE: 2002-12-23				
; PRIOR APPLICATION NUMBER: US/09/290,734				
; PRIOR FILING DATE: 1999-04-13				
; NUMBER OF SEQ ID NOS: 35				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 6				
; LENGTH: 485				
; TYPE: PRT				
; ORGANISM: Bacillus sp.				
US-10-327-837-6				

	Query Match	100.0%	Score 2703	DB 12	Length 485	
	Best Local Similarity	100.0%	Pred. No. 3.8e-241			
	Matches 485	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
Qy	1	HHNGTGTWQYFEWYLPNDGNHNRNLNSDASNLKSGITAVTWIPPAKMGASQNDVGYGA	60			
Db	1	HHNGTGTWQYFEWYLPNDGNHNRNLNSDASNLKSGITAVTWIPPAKMGASQNDVGYGA	60			
Qy	61	YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLKNNGIQVYGDVVNNHKGADATENVRAV	120			
Db	61	YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLKNNGIQVYGDVVNNHKGADATENVRAV	120			
Qy	121	EVFNPNRNQEVGTGYTTTEAWTRFPDPGKGNTHSSFKRWYHFHFDGVDWQDSRLNNRIYKF	180			
Db	121	EVFNPNRNQEVGTGYTTTEAWTRFPDPGKGNTHSSFKRWYHFHFDGVDWQDSRLNNRIYKF	180			
Qy	181	RGHGKAWDWEYDTENGNYDYLMYADIDMDHPPEVNVLENRWGVYNTTGLDGFGRIDAVKH	240			
Db	181	RGHGKAWDWEYDTENGNYDYLMYADIDMDHPPEVNVLENRWGVYNTTGLDGFGRIDAVKH	240			

	Query Match	100.0%;	Score 2703;	DB 12;	Length 485;
	Best Local Similarity	100.0%;	Pred. No. 3.8e-241;		
	Matches 485;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	HHNGTGTMMQYFFWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA	60		
Db	1	HHNGTGTMMQYFFWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA	60		
Qy	61	YDYLDELGEFNKGTVRTKYGTRSQLOAAVTSLLKNGIQVYGDVVMNHKGADATEMVRV	120		
Db	61	YDYLDELGEFNKGTVRTKYGTRSQLOAAVTSLLKNGIQVYGDVVMNHKGADATEMVRV	120		
Qy	121	EVDNNENNOEVTGVTTEAWTPNDPDCGNGTHSSFKPWEVYHFYDGVDDNDOSPRIKNNR	180		


```
RESULT 10
US-09-918-543-12
; Sequence 12, Application US/0918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kiaerulf, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-918-543-12

Query Match          96.7%; Score 2613; DB 9; Length 485;
Best Local Similarity 95.5%; Pred. No. 8.2e-233;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNNRLNSDASNLKSKGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNNRLNSDASNLKSKGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYLGEFNGKGTVRTKYGTRNQLQAAVTSLNKNGIQYVGVVNMHKGADATEMVRV 120
DB 61 YDLYLGEFNGKGTVRTKYGTRNQLQAAVTSLNKNGIQYVGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNQEVTSGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
DB 121 EVNPNRNQEVTSGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPVVNVLNNGWVYNTLTGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPVVNVLNNGWVYNTLTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSATGKNMFVAFWKNDLGAIENYLKTNWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSATGKNMFVAFWKNDLGAIENYLKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIIFNGTVVQRHPHSHAVTFVDNHDQPEEALSFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRNIIFNGTVVQRHPHSHAVTFVDNHDQPEEALSFVEEWFKPLAYALTIRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKYAYGKQNDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKYAYGKQNDYLDHNNIIGWTRGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKAQGVWSDITGNRTGTVTINADGNGNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFMVGRNKAQGVWSDITGNRTGTVTINADGNGNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485

RESULT 11
US-09-925-576C-12
; Sequence 12, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants

RESULT 12
US-10-327-837-24
; Sequence 24, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
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```
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-24

Query Match
Best Local Similarity 96.7%; Score 2613; DB 12; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLYDLGEFQKQGVTRTKYGRSLOQAATVSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFQKQGVTRTKYGRNQLQAANALKSGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNOEVTGEYTTIEATWTRPFGRGNTSHSPKRWYHFDGVDWQSRLLNRIYKF 180
Db 121 EVNPNRNOEVTGEYTTIEATWTKFDPGGRGNTSHSPKRWYHFDGVDWQSRLLNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEPKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEPKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Qy 301 SKSGGNDMNIENGTVVQRHPSHATFVDNHDSPQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGGNDMNIENGTVVQRHPSHATFVDNHDSPQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILKARQYAGKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILKARQYAGKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Qy 481 IWVK 485
Db 481 IWVK 485

RESULT 14
US-10-209-812-5
; Sequence 5, Application US/10209812
; Publication No. US2003008785A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/10/209,812
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/417,359
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-209-812-5

Query Match
96.7%; Score 2613; DB 14; Length 485;
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; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-24

Query Match
Best Local Similarity 95.5%; Pred. No. 8.2e-233;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLYDLGEFQKQGVTRTKYGRSLOQAATVSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFQKQGVTRTKYGRNQLQAANALKSGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNOEVTGEYTTIEATWTRPFGRGNTSHSPKRWYHFDGVDWQSRLLNRIYKF 180
Db 121 EVNPNRNOEVTGEYTTIEATWTKFDPGGRGNTSHSPKRWYHFDGVDWQSRLLNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEPKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEPKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Qy 301 SKSGGNDMNIENGTVVQRHPSHATFVDNHDSPQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGGNDMNIENGTVVQRHPSHATFVDNHDSPQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILKARQYAGKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILKARQYAGKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Qy 481 IWVK 485
Db 481 IWVK 485

RESULT 13
US-10-327-837-26
; Sequence 26, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Biagard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-26

Query Match
96.7%; Score 2613; DB 12; Length 485;
```

Best Local Similarity 95.5%; Pred. No. 8.2e-233; Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;									
Qy	1	HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAWKGASQNDVGYGA	60						
Db	1	HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAWKGASQNDVGYGA	60						
Qy	61	YDLYDLGEFNQKGTVRTKYGTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV	120						
Db	61	YDLYDLGEFNQKGTVRTKYGTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV	120						
Qy	121	EVPNNRNQVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF	180						
Db	121	EVPNNRNQVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF	180						
Qy	181	RHGKAWDEVDTEGNYDYLMDADIMDHPVNVNELRWGVMYTTTLGLDGFRIIDAVKH	240						
Db	181	RHGKAWDEVDTEGNYDYLMDADIMDHPVNVNELRWGVMYTTTLGLDGFRIIDAVKH	240						
Qy	241	IKYSFTRDWINHVRSAITGKMFPAVAEFWKNDLGAIENTYLOKTNWNHVSFDPVPLHYNLYNA	300						
Db	241	IKYSFTRDWINHVRSAITGKMFPAVAEFWKNDLGAIENTYLOKTNWNHVSFDPVPLHYNLYNA	300						
Qy	301	SKSGGNYDMRNI FNGTIVVQRHPHSHAVTFVDNHDSSQPEEALSFVBEWFKPLAYALTLTRE	360						
Db	301	SKSGGNYDMRNI FNGTIVVQRHPHSHAVTFVDNHDSSQPEEALSFVBEWFKPLAYALTLTRE	360						
Qy	361	QGYPSVFYGDYIGIPTHGVPAMRSKIDPILFARQKYAYGKONDYLDHNNIIGWTRREGNTA	420						
Db	361	QGYPSVFYGDYIGIPTHGVPAMRSKIDPILFARQKYAYGKONDYLDHNNIIGWTRREGNTA	420						
Qy	421	HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS	480						
Db	421	HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS	480						
Qy	481	IWNK 485							
Db	481	IWNK 485							
Search completed: October 7, 2004, 00:57:33 Job time : 54.4478 secs									

Qy	121	EVPNNRNQVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF	180						
Db	121	EVPNNRNQVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF	180						
Qy	181	RHGKAWDEVDTEGNYDYLMDADIMDHPVNVNELRWGVMYTTTLGLDGFRIIDAVKH	240						
Db	181	RHGKAWDEVDTEGNYDYLMDADIMDHPVNVNELRWGVMYTTTLGLDGFRIIDAVKH	240						
Qy	241	IKYSFTRDWINHVRSAITGKMFPAVAEFWKNDLGAIENTYLOKTNWNHVSFDPVPLHYNLYNA	300						
Db	241	IKYSFTRDWINHVRSAITGKMFPAVAEFWKNDLGAIENTYLOKTNWNHVSFDPVPLHYNLYNA	300						
Qy	301	SKSGGNYDMRNI FNGTIVVQRHPHSHAVTFVDNHDSSQPEEALSFVBEWFKPLAYALTLTRE	360						
Db	301	SKSGGNYDMRNI FNGTIVVQRHPHSHAVTFVDNHDSSQPEEALSFVBEWFKPLAYALTLTRE	360						
Qy	361	QGYPSVFYGDYIGIPTHGVPAMRSKIDPILFARQKYAYGKONDYLDHNNIIGWTRREGNTA	420						
Db	361	QGYPSVFYGDYIGIPTHGVPAMRSKIDPILFARQKYAYGKONDYLDHNNIIGWTRREGNTA	420						
Qy	421	HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS	480						
Db	421	HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS	480						
Qy	481	IWNK 485							
Db	481	IWNK 485							

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-13
Perfect score: 2703
Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGWNFSVNGSGSVSIWNK 485

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2410	89.2	516	2	O82839
2	1947	72.0	533	2	Q9AQ34
3	1941	71.8	513	16	O81YJ4
4	1929	71.4	513	16	O81AS4
5	1888.5	69.9	613	2	Q59222
6	1878	69.5	519	2	Q9RQ78
7	1876.5	69.4	529	2	O31193
8	1871.5	69.2	521	2	P71034
9	1871.5	69.2	549	2	Q9KWY6
10	1802.5	66.7	501	2	Q93148
11	1570.5	58.1	507	16	Q87HG6
12	1360	50.3	493	2	Q03657
13	1339	49.5	481	16	Q89YF1
14	1280.5	47.7	488	16	Q8EOM2
15	1287.5	47.6	486	16	Q8D708
16	1283.5	47.5	488	16	Q8E696

17 1280 47.4 484 16 Q97Q49 streptococc
18 1278 47.3 484 16 Q8DPC8 streptococc
19 1275 47.2 492 16 Q8YU21 anabaena sp
20 1259.5 46.6 486 2 O68875 streptococc
21 1250.5 46.3 484 2 O50583 streptococc
22 1246.5 46.1 485 2 Q53786 streptococc
23 1139 42.1 491 16 Q9CG59 lactococcu
24 1125 41.6 506 16 Q8U916 agrobacteri
25 1064 39.4 494 16 Q8Z5S5 salmonella
26 1054 39.0 495 16 Q8XBB6 escherichia
27 1050 38.8 495 16 Q8FGL8 escherichia
28 1043 38.6 495 16 Q7UAB0 shigella fl
29 1041 38.5 495 16 Q83R40 shigella fl
30 1033.5 38.2 529 3 Q877B1 aspergillus
31 474.5 17.6 461 1 O33476 pyrococcus
32 474.5 17.6 461 1 O8NKR4 thermococcu
33 459 17.0 469 1 O50200 thermococcu
34 456 16.9 432 14 Q8JZK3 uncultured
35 453.5 16.8 461 1 Q8NKR5 thermococcu
36 450.5 16.7 460 1 Q9P9L0 pyrococcus
37 450.5 16.7 460 1 O08452 pyrococcus
38 450.5 16.7 473 17 Q8U319 pyrococcus
39 442 16.4 457 1 Q93647 thermococcu
40 311.5 11.5 482 2 Q60051 thermocactin
41 285 10.5 504 1 Q60224 natronococ
42 281.5 10.4 421 10 Q7X9T1 phaseolus a
43 280 10.4 420 10 Q92P43 phaseolus v
44 279.5 10.3 906 10 Q8LQK4 oryza sativ
45 279 10.3 424 10 Q8LP27 pharbitis n

ALIGNMENTS

RESULT 1

O82839 ID O82839 PRELIMINARY; PRT; 516 AA.

AC O82839
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN=KSM-1378;
RX MEDLINE=98342096; PubMed=9675143;
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding.";
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL; AB008763; BAA32431.1; -
DR HSPB; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 89.2%; Score 2410; DB 2; Length 516;

Best Local Similarity 86.4%; Pred. No. 6.2e-146;

Matches 419; Conservative 36; Mismatches 30; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60

Db 32 HHNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGTQNDVGYGA 91

```
QY 61 YDLYDLGEFNQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 92 YDLYDLGEFNQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 151
QY 121 EVNPNRNQEVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYK 180
DB 152 EVNPNRNQEVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYK 211
QY 181 RHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRWGVWYTTGLDGRIDAVKH 240
DB 212 RGTGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRWGVWYTTGLDGRIDAVKH 271
QY 241 IKYSFTDRDINHVRSAVKMFAVAEPMKNDLGAENYLOKTNWHSVFDVPLHYNLYNA 300
DB 272 IKYSFTDRDINHVRSAVKMFAVAEPMKNDLGAENYLOKTNWHSVFDVPLHYNLYNA 331
QY 301 SKSGGNYDMRNIFNGTVVVRHPSHVAFTVDNHDSPQBEALESFVEEWFKPLAYALTITRE 360
DB 332 SKSGGNYDMRNIFNGTVVVRHPSHVAFTVDNHDSPQBEALESFVEEWFKPLAYALTITRE 391
QY 361 QGYPSPYGYDYGIPTHGVPMESKIDPILAEARKYAGKQNDYLDHNNIIGWTRGNTA 420
DB 392 QGYPSPYGYDYGIPTHGVPMESKIDPILAEARKYAGKQNDYLDHNNIIGWTRGNTA 451
QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 480
DB 452 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 511
QY 481 IWVKNK 485
DB 512 VVWKQ 516

RESULT 2
Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amyrase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
RT KSM B-404."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amyrase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR Pfam; PF00128; alpha-amyrase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 72.0%; Score 1947; DB 2; Length 533;
Best Local Similarity 69.4%; Pred. No. 2.4e-116;
Matches 335; Conservative 62; Mismatches 82; Indels 4; Gaps 2;

QY 6 NGTMQYFEWYLPNDGNHNLNSDASNLKSGITAYVIPPWKASQNDVGAYDLYD 65
DB 52 NGTMQYFEWYLPNDGNHNLRLRTDAENLAKGITSVWIPPAYKGTQNDVGAYDLYD 111
QY 66 LGFENQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 125
DB 112 LGFENQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 171
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QY 126 NRNQEVTGEYTIETAWTRDFPGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKFRGHGK 185
DB 172 NRNVEVSGDYEISAWTGFNFGDGSYSNFKWKYHFDGTDMDGKCL-NRIYKFRGIGK 230
QY 186 AMDWEVDTEGNGYDLYMADIDMDHPEVNVNLRWGVWYTTGLDGRIDAVKHKYSF 245
DB 231 AMDWEVSSGNGYDLYMADIDMDHPEVNVNLRWGVWYTTGLDGRIDAVKHIDHEY 290
QY 246 TRDWNHVSATGKMFVAEPMKNDLGAENYLOKTNWHSVFDVPLHYNLYNASKSGG 305
DB 291 LRDWNHVSATGKMFVAEPMKNDLGAENYLOKTNWHSVFDVPLHYNLYNASKSGG 350
QY 306 NYDMRNIFNGTVVVRHPSHVAFTVDNHDSPQBEALESFVEEWFKPLAYALTITRE 365
DB 351 NYDMRNIFNGTVVVRHPSHVAFTVDNHDSPQBEALESFVEEWFKPLAYALTITRE 410
QY 366 VYGYDYGIPTHGVPMESKIDPILAEARKYAGKQNDYLDHNNIIGWTRGNTAHP 422
DB 411 VYGYDYGIPTHGVPMESKIDPILAEARKYAGKQNDYLDHNNIIGWTRGNTAHP 470
QY 423 NSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 482
DB 471 NSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGSGVS 530
QY 483 VNK 485
DB 531 VQR 533

RESULT 3
Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amyrase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Routs D.E., Eisen J.A., Gill S.R.,
RA Holtzapfel E.K., Okstad O.A., Helgason E., Bilstone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.P.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423.81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amyrase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR Pfam; PF00128; alpha-amyrase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 71.8%; Score 1941; DB 16; Length 513;
Best Local Similarity 69.4%; Pred. No. 5.6e-116;
Matches 335; Conservative 63; Mismatches 81; Indels 4; Gaps 2;
```

QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGAYDLYD 65
 DB 32 NGTLMQYFEWYAPSDRHNHNRRLRTDAENLAQKSGITSVIPPAKGTQNDVGYGAYDLYD 91
 QY 66 LGFENQKGTVRTKYGTSQLOAAVTSLNKNGIQYQYGVVNMHKGADATEMVRVAVENPN 125
 DB 92 LGFENQKGTVRTKYGTKAQLKSALEALHKQNDIDYQYGVVNMHKGADYTTETVTAVEVDN 151
 QY 126 NRQEVGTGEYTIETAWTRFDPGRGNTHSSFKRWYHFDGVDWDSRRLNRIYKFRGHGK 185
 DB 152 NRNVESGDEYISAWTGFNPFGRGDNYSNFKWKYHFDGTDWDEGRKL-NRIYKFRGIGK 210
 QY 186 AWDWEVDTEGNVDYLMYADIDMDHPEVNMELRWNGVYNTLGLDGFRIIDAVKHIIKYSF 245
 DB 211 AWDWEVSSENGVDYLMYADIDFDPDVANEMKNGTWYANELNLDGFRIDAVKHIDHEY 270
 QY 246 TRDWINHVRSGATGNMFAVAFWKNDLGAIENTYLOKTNMHSVDFDPLHYNLYNASKSGG 305
 DB 271 LRDMVNHVRQOTGKEMFTVAEYQNDIQTLNNYLAKVYNNQSVFDPALHYNFHYASKNG 330
 QY 306 NYDMRNIFNGTVQORHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOGYPS 365
 DB 331 NYDMRNILNGTVQNHQPALAVTLVENHDSQPSLESVSWPFPKPLAYAFILTRAEGYPS 390
 QY 366 VFYGDYVGI---PTHGVPMRSKIDPILAEARQYAYGKQNDYLDHNNIIGWTRGNTAHP 422
 DB 391 VFYGDYVGTSGNSYEIPALKDKIDPILTARKNFAYGTQRYDLDPDVIGWTRGDSVHA 450
 QY 423 NSGLATIMSDGAGSKWVFGRNKGQVMSDITGNRTGTTVINADGNFVNGSGSVSIW 482
 DB 451 NSGLATILISDGPCKWMDVGKKNAGEVWHDMTGNQNTVTINKDGWQFVSGSVSIY 510
 QY 483 VNK 485
 DB 511 VQO 513

RESULT 4

Q81AS4 PRELIMINARY; PRT; 513 AA.
 AC Q81AS4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glucan 1,4-alpha-maltohexaoidase (EC 3.2.1.98).
 GN BC3482.
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 Overbeek R., Kyrpides N.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 Bacillus anthracis";
 RL Nature 423:87-91 (2003).
 DR EMBL; AE017009; AAP10417.1; --
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Glycosidase; Hydrolase; Complete proteome.
 SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF9F9F6 CRC64;

Query Match

71.4%; Score 1929; DB 16; Length 513;

Best Local Similarity 68.7%; Pred. No. 3.3e-115;
 Matches 332; Conservative 62; Mismatches 85; Indels 4; Gaps 2;
 QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGAYDLYD 65
 DB 32 NGTLMQYFEWYAPSDRHNHNRRLRTDAENLAQKSGITSVIPPAKGTQNDVGYGAYDLYD 91
 QY 66 LGFENQKGTVRTKYGTSQLOAAVTSLNKNGIQYQYGVVNMHKGADATEMVRVAVENPN 125
 DB 92 LGFENQKGTVRTKYGTKAQLKSAIDALHKKNDIDYQYGVVNMHKGADYTTETVTAVEVDP 151
 QY 126 NRQEVGTGEYTIETAWTRFDPGRGNTHSSFKRWYHFDGVDWDSRRLNRIYKFRGHGK 185
 DB 152 NRNVESGDEYISAWTGFNPFGRGDSYSNFKWKYHFDGTDWDEGRKL-NRIYKFRGIGK 210
 QY 186 AWDWEVDTEGNVDYLMYADIDMDHPEVNMELRWNGVYNTLGLDGFRIIDAVKHIIKYSF 245
 DB 211 AWDWEVSSENGVDYLMYADIDFDPDVANEMKNGTWYANELNLDGFRIDAVKHIDHEY 270
 QY 246 TRDWINHVRSGATGNMFAVAFWKNDLGAIENTYLOKTNMHSVDFDPLHYNLYNASKSGG 305
 DB 271 LRDMVNHVRQOTGKEMFTVAEYQNDIQTLNNYLAKVYNNQSVFDPALHYNFHYASKNG 330
 QY 306 NYDMRNIFNGTVQORHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOGYPS 365
 DB 331 NYDMRNILNGTVQNHQPALAVTLVENHDSQPSLESVSWPFPKPLAYAFILTRAEGYPS 390
 QY 366 VFYGDYVGI---PTHGVPMRSKIDPILAEARQYAYGKQNDYLDHNNIIGWTRGNTAHP 422
 DB 391 VFYGDYVGTSGNSYEIPALKDKIDPILTARKNFAYGTQRYDLDPDVIGWTRGDSVHA 450
 QY 423 NSGLATIMSDGAGSKWVFGRNKGQVMSDITGNRTGTTVINADGNFVNGSGSVSIW 482
 DB 451 NSGLATILISDGPCKWMDVGKKNAGEVWYDITGNQNTVTINKDGWQFVSGSVSIY 510
 QY 483 VNK 485
 DB 511 VQO 513

RESULT 5
 Q59222 PRELIMINARY; PRT; 613 AA.
 AC Q59222;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Alpha-amylase (EC 3.2.2.1).
 GN AMY.
 OS Bacillus sp. TS-23.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=38441;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=TS-23;
 RA Lin L.-L., Chu W.S., Hsu W.H.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U22045; AAA63900.1; --
 DR HSP; P06278; IYUS.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR002044; CBD_4.
 DR Pfam; PF00128; alpha-amylase; 13.
 DR Pfam; PF006046; Glyco_hydro_1.
 DR Pfam; PF00686; CBM_20; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 KW Glycosidase; Hydrolase.

SQ	SEQUENCE	613 AA; 69537 MW; 14684A30FC2895E8 CRC64;	
QY	Query Match	69.9%; Score 1888.5; DB 2; Length 613;	
Db	Best Local Similarity	68.1%; Pred. No. 1.6e-112; Indels 1; Gaps 1;	
Matches	327; Conservative	66; Mismatches 86;	
QY	6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLYD 65		
Db	36 NETMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLYD 95		
QY	66 LGFBNQKGTVRTKYSQLOAAVTSLNKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 125		
Db	96 LGFBNQKGTVRTKYSQLOAAVTSLNKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 155		
QY	126 NRNOEVTGEYTIKAWTRFDPFGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 185		
Db	156 NRNOEVTGEYTIKAWTRFDPFGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 214		
QY	186 AWDWEVDTEGNYDYLMDADIDMDHPEVNVNLELNWGVYVNTLGLDGFRIIDAVKHIKYSF 245		
Db	215 AWDWEVDTEGNYDYLMDADIDMDHPEVNVNLELNWGVYVNTLGLDGFRIIDAVKHIKYSF 274		
QY	246 TRDWINHVSATGKNMFAVAFKNDLGAENLYQKTNHNSVDFVPLHLYNLYNASKSG 305		
Db	275 FPDWLTAVRQTKNLFVAGFEFWSYDVKLNHNTITKNGSMSLFDAPLHNFYTASKSG 334		
QY	306 NYDMRNIFNGTVVQRHPSHAFTVDNHDQPEEALSFVEWFKPLAYALTLTREQGYPS 365		
Db	335 YFDMRYLLNLTWKQDPSLAVTLVDNHDTPGQSLQSWEPFKPLAYAFILTRQGYPC 394		
QY	366 VFYGDYGGIPTHGVPMRSKIDPILKARQKYAYGKQNDYLDHNNIIGWTRGNTAHPSNG 425		
Db	395 VFYGDYGGIPKYNIPGLKSKIDPILKARQKYAYGKQNDYLDHNNIIGWTRGNTAHPSNG 454		
QY	426 LATIMSDGAGSKMFWGRNKAQVWSDTGNRTGTVTINADGWNFSVNGGVSIVWYK 485		
Db	455 LAALITDGPCKGSKMFWGRNKAQVWSDTGNRTGTVTINADGWNFSVNGGVSIVWYK 514		
RESULT 6			
ID	Q9RQ78 PRELIMINARY; PRT; 519 AA.		
AC	Q9RQ78		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Raw starch digesting amylase precursor.		
OS	Cytophaga sp.		
OC	Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;		
OC	Flexibacteraceae; Cytophaga.		
OX	NCBI_TaxID=29535;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Jeang C.L., Chen L.S., Chen M.Y.;		
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF067653; AAF00567.1; -.		
DR	HSSP; P06278; 1VJS.		
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_ami cat.		
DR	InterPro; IPR006589; Alp_ami cat sub.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
KW	Signal.		
FT	SIGNAL		
FT	CHAIN		
SQ	SEQUENCE 519 AA; 58337 MW; 356B88A4DF98B163 CRC64;		
Query Match	69.5%; Score 1878; DB 2; Length 519;		
Best Local Similarity	67.4%; Pred. No. 6e-112;		
Matches	326; Conservative 71; Mismatches 83; Indels 4; Gaps 2;		
QY	6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLYD 65		
Db	37 TNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLY 96		
QY	65 DLGEFNQKGTVRTKYSQLOAAVTSLNKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 124		
Db	97 DLGEFNQKGTVRTKYSQLOAAVTSLNKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 156		
QY	125 NRNOEVTGEYTIKAWTRFDPFGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 184		
Db	157 NRNOEVTGEYTIKAWTRFDPFGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 215		
QY	185 KAWDWEVDTEGNYDYLMDADIDMDHPEVNVNLELNWGVYVNTLGLDGFRIIDAVKHIKYS 244		
Db	216 KAWDWEVDTEGNYDYLMDADIDMDHPEVNVNLELNWGVYVNTLGLDGFRIIDAVKHIKYS 275		
QY	245 FTRDWINHVSATGKNMFAVAFKNDLGAENLYQKTNHNSVDFVPLHLYNLYNASKSG 304		
Db	276 FLKDWVDNARAATGKEMFTVGEYQNDLGAENLYQKTNHNSVDFVPLHLYNLYNASKSG 335		
QY	305 GNYDMRNIFNGTVVQRHPSHAFTVDNHDQPEEALSFVEWFKPLAYALTLTREQGYPS 364		
Db	336 GNYDMRNIFNGTVVQRHPSHAFTVDNHDQPEEALSFVEWFKPLAYALTLTREQGYPS 395		
QY	365 SVFYGDY--GIPTHGVPMRSKIDPILKARQKYAYGKQNDYLDHNNIIGWTRGNTAH 421		
Db	396 SVFYGDY--GIPTHGVPMRSKIDPILKARQKYAYGKQNDYLDHNNIIGWTRGNTAH 455		
QY	422 PMSGLATIMSDGAGSKMFWGRNKAQVWSDTGNRTGTVTINADGWNFSVNGGVSIG 481		
Db	456 AKSGLATIMSDGAGSKMFWGRNKAQVWSDTGNRTGTVTINADGWNFSVNGGVSIG 515		
QY	482 WYK 485		
Db	516 WYK 519		
RESULT 7			
ID	O31193 PRELIMINARY; PRT; 549 AA.		
AC	O31193		
DT	01-JAN-1998 (TrEMBLrel. 05, Created)		
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Alpha amylase.		
OS	AMI.		
OC	Bacillus stearothermophilus.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.		
OX	NCBI_TaxID=1422;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=ATCC 31195;		
RL	da Silva A.C.R., Fernandes E., Pueyo M.T.;		
DR	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF032864; AAB86961.1; -.		
DR	PIR; A54541; A54541.		
DR	HSSP; P06278; 1VJS.		
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_ami cat.		
DR	InterPro; IPR006589; Alp_ami cat sub.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
SQ	SEQUENCE 549 AA; 62651 MW; 2CA689BDACC4D262 CRC64;		
Query Match	69.4%; Score 1876.5; DB 2; Length 549;		
Best Local Similarity	67.4%; Pred. No. 8e-112;		
Matches	322; Conservative 75; Mismatches 80; Indels 1; Gaps 1;		

[illegible]

RESULT 8

P71034	PRELIMINARY;	PRT;	521 AA.
ID	P71034		
AC	P71034;		
DT	01-FEB-1997 (TrEMBLrel. 02, Created)		
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Alpha-amylase precursor.		
OS	Bacillus sp. MK 716.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
NCBI_OX	NCBI_TaxID=54116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MK 716;		
RA	Sidhu G.S., Chakrabarti T.;		
RT	"Molecular cloning and expression of the gene encoding for		
RT	thermostable alpha-amylase of a thermophilic bacterial isolate.";		
RL	Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; U75445; AAB18785.1; --		
DR	HSP; P06278; 1VJS.		
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	Interpro; IPR006047; Alpha_amyl_cat.		
DR	Interpro; IPR006589; Alp_amyl_cat_sub.		
DR	Interpro; IPR006046; Glyco_hydro_I3.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
DR	Signal.		
FT	SIGNAL	1	34
FT	CHAIN	35	521
FT	SEQUENCE	521 AA; 59311 MW;	5612A8859D922E1 CRC64;
SQ	SEQUENCE	521 AA; 59311 MW;	5612A8859D922E1 CRC64;

Qy	66	LGEFNQKGTVRTKYGTRSQLQAAVYTSLNKNGIQVYGDVNMHKGADATMVRVAVEVNP	125
Db	99	LGEFNQKGAVRTKYGTRQAQYLQAIQAHAAGAQVYVDFDHKGGADGTWVDVAVEVNP	158
Qy	126	NRNQEVTEGYTIEAWTHPDPGRGNTHSSFKWRWVHFDGVQDWDQSRLLNNRILYKPRGHOK	185
Db	159	DRNQIESGTQIQIAWTTFDPGRGNTHSSFKWRWVHFDGVQDWDSEKRL-SRIYKPRGIGK	217
Qy	186	AWDEWVDTENGNDYDLYMADIDMDHPEVYNELRNKGVWYVNTLGLDGRFIDAVKHIKYSF	245
Db	218	AWDEWVDTENGNDYDLYMADIDMDHPEVYTELKNWGWYVNTNIDGRFLDAVKHIKFSF	277
Qy	246	TRDWINVRSATGKMFPAFAEFKQNDLCAIENYLQKTWNHNSVFVPLHNYLYNASKSGG	305
Db	278	FPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTINGTMSLDFAPLHNKPYTASKSGG	337
Qy	306	NYDMRNIENGHVQVRHPSHATVFDNHDSDQPEALESFEVEWFKPLAYALTITRQGYPS	365
Db	338	AFDMRTLMTNLMDKQDPTLAVTFVDNHDHTEPQALQSWDPMFKPLAYAFILTRQEGYPC	397
Qy	366	VFYGDYYGIPTHGVPAMRSKIDPILAEARKYAYQKNDYLDHNNIIGWTRGENTAHPSNG	425
Db	398	VFYGDYYGIQYNIPLSKSIDPILIARRDYAYGTQHDYLDHSDIIGWTRGVTKEPKSGG	457
Qy	426	LATIMSDGAGSKMVFGRNKAQGVWSDITGNRTGTVTINADGWNFNFSVNGSGSVIWV	483
Db	458	LAALITDPGSGKMWYVGHQAGKVFYDLTGNRSDTIVTINSIDGWGEFKVNGSGSVWV	515

RESULT 9

Q9KWKY6 PRELIMINARY; PRT; 549 AA.
AC Q9KWKY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase [EC 3.2.1.1].
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
CX NCBI_TaxID=1422;
RN [1]
RZ SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSP; P06278; 1VJS.
DR GO; GO:0004356; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amy_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF001128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase.
KW SEQUENCE 549 AA; 62582 MW; 8DA3B666DF9120BCE CRC64;
SQ

[illegible]

Db	159	DRNQELSGYQ	QAWTKFPFGKNTYSEFKWRYHFDGVDWDESRKL-SRIYKFRGICK	217			
Qy	186	AWDWEYDVTENGNY	DYLMYADIMDHPPEVYNELRNWGVYNTLTGLDGFRIADVKHIKYSF	245			
Db	218	AWDWEYDVTENGNY	DYLMYADLMDHPPEVTELKNWGWYVNTTNIDGFRLDADVKHIKFSF	277			
Qy	246	TRDWINHVSATGKM	FAVAEFKNDLGAENLYOKTNWNHSDYDPLHYNLNASKSGG	305			
Db	278	FPDWLSYVSRSQ	KPLFTVGEYWSYDINKLHNITTINGTMSLFDAPLHNKFTASKSGG	337			
Qy	306	NYDMRNIENGTV	VORHPHSHAVTFVDNHDSDPEALESFVZEWEFKPLAYALTLTREOCYPS	365			
Db	338	AFDMRTLMTNL	MKOQPTLAVTFVDNHDTEFGALQSWDWPWKPLAYAFILTRQSGYPG	397			
Qy	366	VFYGDYIGITHGP	PAWRSKIDPILFEARQKYAYGQNQYLDHNNIIGWTREGNTAHPNSG	425			
Db	398	VFYGDYIGIPQ	YNIPSLKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTREGVTEKPGSG	457			
Qy	426	LATIMSDGAGGSK	WMFVGRNKAQVWSDITGNRTGTVTTINADCGWSPSVNGGVSIVW	483			
Db	458	LAALITDGPFGSK	WMYVQKHAGKVFDLTGNRSDTVTITSDGWGEFKVNGGVSVMW	515			
RESULT 10							
Q93148							
ID	Q93148	PRELIMINARY; PRT; 501 AA.					
AC	Q93148;						
DT	01-DEC-2001	(T-EMBLrel. 19, Created)					
DT	01-DEC-2001	(T-EMBLrel. 19, Last sequence update)					
DT	01-JUN-2003	(T-EMBLrel. 24, Last annotation update)					
DE	Amylase.						
GN	AMEYK38.						
OS	Bacillus sp. KSM-K38.						
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.						
OX	NCBI_TaxID=129736;						
RP	[1]						
RN	SEQUENCE FROM N. A.						
RC	STRAIN=KSM-K38;						
RA	Hayashi Y.;						
RT	"Isolation of a new Bacillus alpha-amylase."						
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AB051102; BAB71820.1; -.						
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.						
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.						
DR	InterPro; IPR006047; Alpha amyl cat.						
DR	Pfam; PF00128; alpha-amylase; 1.						
SEQ	SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;						
Query Match							
Best Local Similarity 64.0%; Pred. No. 3.8e-107; DB 2; Length 501;							
Matches 309; Conservative 78; Mismatches 93; Indels 3; Gaps 2;							
Qy	3	NGTNGTMMQYF	EWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKGASQNDVGYGAYD	62			
Db	22	DGLNGTMMQYF	EWLENDGQHNRKLDHDAALSAGITAIWIPYKGNQADVGYGAYD	81			
Qy	63	LYDLGEFNQKGT	VRTKYGTGTSQLQAAVTSLKNGIQYGVGVVNMHKGADATEWRAVEV	122			
Db	82	LYDLGEFNQKGT	VRTKYGTGAQLERAIGSLKNSDINVYGDVVMHKGADPTEAVQAVQV	141			
Qy	123	NNNRNQEVGT	EYTIETAWTRPDFRCGRNTHSSFKWRVHFQGVQDWDQSRRLNRIYKPRG	182			
Db	142	NPTNRWQDIS	GAYTIIDAWTGDFDGSRRNAYSDFKWRVHFHFGVQDWDQ-RYQENHIFRPN	200			
Qy	183	HGKAWDNEVD	TENGNYDLYMADIMDHPPEVYNELRNWGVYNTLTGLDGFRIADVKHIK	242			
Db	201	TN--	WNWRVDEENGNYDILGSNIDFSHPVQDELKDWGSWFTDELDDLGYRLDAIKHP	258			
Qy	243	YSFTRDWINH	VSATGKNMFABAFAFWKNDLGAENLYOKTNWNHSDYDPLHYNLNASK	302			
Db	259	FWTSDWVR	HORNEADQDLFVVGWYKQDDVGALEFYLDENWWSLFDVPLNYTFYRASQ	318			


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Db 322 SGNFTDMEQWNTLMKONPVKAVTLVNHDTQPLQALESTVDWMFKPLAYAIFLLRREG 381
Qy 363 YPSVFGDYGG-----IPTHGVPAMRSKIDPILAEARQYAYGKQNDYLDHNIIGW 413
Db 382 YPSVFYADYGAQYSDKGNINMAKVP-----YIELVTLRKEYAYGKQNSYLDHWDVLGW 437
Qy 414 TREGTAHPNSGLATIMSDGAGGSKMVFGRNKAQVMSDITGNRTGTTINADGWNFS 473
Db 438 TREGDAHPNS-MAVIMSDGPGTKMYTGKSTRYV--DKLGIRTEEVWTDANGWAEFP 494
Qy 474 VNGGSVSIWV 483
Db 495 VNGGSVSVWV 504

RESULT 12
Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657,
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Glyco_hydro_13.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; PFCCD2F805BB4694 CRC64;

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Query Match 50.3%; Score 1360; DB 2; Length 493;
Best Local Similarity 50.9%; Pred. No. 5.9e-79;
Matches 245; Conservative 78; Mismatches 150; Indels 8; Gaps 3;

Qy 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVMIPPAMKASQNDVGYGAYDLYD 65
Db 4 NHTMMQYFEWHLAAGDGHMKELAEMAPLAKAGIDTVWVPVTKAVSAEDTGYGYDLYD 63

Qy 66 LGFENQKGTVRTKYGTSQLOAAVTSLNKNGIQYGVDMVNMHKGADATMVRVAVNPN 125
Db 64 LGFEDQKGTVRTKYGTSQLOAAVTSLNKNGIQYGVDMVNMHKGADATMVRVAVNPN 123

Qy 126 NRNQVTEGTYTIEAWTRFDPFGCRNTHSSFKWRNYHFDGVDWDQSRRLNRIYKFRGHGK 185
Db 124 DRTKEISPEPFEIGTWKTFPPGRGDQVSSFKWNEHFNGTDFD-AREERTGVFFRAGENK 182

Qy 186 AWDMEVTEGNYDYLMAVDIMDHPVNMELRWNVYNTTLGLDGPRIIDAVKHICYSF 245
Db 183 KWNENVDDEFGNYDYLMAFNIDYNHDPVVRMIDWKGWLIDTLQCGGFLRDAIKHINHEP 242

Qy 246 TRDWINHVRSGATGKMFVAFWKNLDGAIENYLOKTNWNHNSVDFVPLHLYNLYNASKSGG 305
Db 243 IKEFAEAMIRKRGQDFYIVGFWNSNLDACREFLDTVQIDLDLVSILHYKLHEASLGR 302

Qy 306 NYDMRNTFNGTVVORHPSHVTVDNHDSPHEALESFVBEWFKPLAYALTLTREOGYPS 365
Db 303 DFDLSKIFDDTLVQTHPTHTAVTFVDNHDSPHEALESWIGDWFKPSPAYALTLLRRDGYPV 362

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Qy 366 VFYGDYGI-----PTHGVPAMRSKIDPILAEARQYAYGKQNDYLDHNIIGTREGNTAH 421
Db 363 VFYGDYGI-----KKEILDILLSARCNKAYGEQEDYFDHANTIGWVRGVEI 419
Qy 422 PMSGGLATIMSDGAGGSKMVFGRNKAQVMSDITGNRTGTTINADGWNFSVNGSGSVI 481
Db 420 ESGGCAVVISNGDGEKRMFIEGHRAGEVWVDLTAKSCDDQITIEEDGWATPHVCGGGSV 479
Qy 482 W 482
Db 480 W 480

RESULT 13
Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI,
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

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Query Match 49.5%; Score 1339; DB 16; Length 481;
Best Local Similarity 49.8%; Pred. No. 1.5e-77;
Matches 239; Conservative 86; Mismatches 153; Indels 2; Gaps 2;

Qy 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVMIPPAMKASQNDVGYGAYDLYD 65
Db 3 NGVMMQYFEWHLPNDGKLMKQIKEDALHLHDIGTAVMIPPAYKADQEDGYATYDLYD 62

Qy 66 LGFENQKGTVRTKYGTSQLOAAVTSLNKNGIQYGVDMVNMHKGADATMVRVAVNPN 125
Db 63 LGFEDQKGTVRTKYGTSQLOAAVTSLNKNGIQYGVDMVNMHKGADATMVRVAVNPN 122

Qy 126 NRNQVTEGTYTIEAWTRFDPFGCRNTHSSFKWRNYHFDGVDWDQSRRLNRIYKFRGHGK 185
Db 123 ERTKALGEPFETIQGTGYSPHGRKDKHSDFKWYHFGSTGTFDQDAQK-RSGVVFQSGEK 181

Qy 186 AWDMEVTEGNYDYLMAVDIMDHPVNMELRWNVYNTTLGLDGPRIIDAVKHICYSF 245
Db 182 AWSGVDSENGNYDYLMAVDIMDHPVNMELRWNVYNTTLGLDGPRIIDAVKHICYSF 241

Qy 246 TRDWINHVRSGATGKMFVAFWKNLDGAIENYLOKTNWNHNSVDFVPLHLYNLYNASKSGG 305
Db 242 VAQFLDAVRSEGRNDFVAVGVEWNGDLEALDAYIEAVGHKYNLFDVPLHLYNMFQASQEGK 301

Qy 306 NYDMRNTFNGTVVORHPSHVTVDNHDSPHEALESFVBEWFKPLAYALTLTREOGYPS 365
Db 302 DYDLRLDKDTLVBHHPDLAVTIVDNHDTORGSSLESNVEDWFKPLAYGLTLLMKEGYPC 361

Qy 366 VFYGDYGIPTHGVPAMRSKIDPILAEARQYAYGKQNDYLDHNIIGTREGNTAHPSNG 425

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362 LFYGDYVIGKEKSPHTRI-IDILLDARRKAYAGDQTEYFDPHSTTGFIQTGDEEHGSG 420
426 LATIMSDGAGGSKWFMVGRNKAGQVMSDITNGTGTVTINADGWNFSVNGSVSIWVVK 485
421 LVFLMSNDEAGSKIMSLGEXKHKEVWHEITGTSISEEITLDEEGNGBFVSERNLAVVVK 480

RESULT 14
Q8E0M2 PRELIMINARY; PRT; 488 AA.
AC Q8E0M2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha amylase family protein.
GN SAG0708.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eissen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AB014223; AAM99595.1; -.
DR TIGR; SAG0708; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF001128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 56555 MW; 57249E354B2F053E CRC64;

Query Match 47.7%; Score 1290.5; DB 16; Length 488;
Best Local Similarity 48.8%; Pred. No. 1.9e-74;
Matches 23; Conservative 82; Mismatches 158; Indels 9; Gaps 5;

QY 5 TNGTMMQYFEWYLPNDGNHNRNLNSDASNIKSGKITAVWIPPAWKASQNDVGYGVDLY 64
DB 2 TNELIMQAFEWYLPDSDGNHKKLEESIDLKLGISKIMLPAPKGTSSDDVGYGYDLF 61
QY 65 DLGEFNQKGTVRTKYGTRSQLQAATVSLKNGIQVYGDVVMNHKGADATEMVRVAVNP 124
DB 62 DLGEFDQNGTIRTKYGRKEEYLKILSKANGIKPFADIVLNHANGDHEKGFQVVKNP 121
QY 125 NNRNOEVTGYTTEAWTRFPDPPGRGNTHSGFKRWYHFGDWDQSRRLNLR--IYKFRG 182
DB 122 ENRQALSEPYEIEGWTGTFDPPGRQGEYDFPKWHYHFTGLDYDAK---NNEITDFMVG 178
QY 183 HGKAW--DWEVDTENGNYDILMYADI DMHDPVVMNELNMGVWYNTLTGLDGRIDAVKH 240
DB 179 DNKGWADDLIDDENGFNFDLYMYNDIDFKGPEVINKLQDWAQWFIETTGIEGRFLDAVKH 238
QY 241 IKYSFTRDWINHVSATGKNMFAVEAEKQNDLGAENYLOKTNWNHVSFVDVPLHNLVNA 300
DB 239 IDSFYIQTFFINDIRTKIKPDLEVFGEYKWSQTSNKOYLEATQFQSLVDVTLHNFDA 298
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301 SKSGGNYDMRNTFNGTIVORHPSHAVTVFDNHDSPBEALESFVEWFKPLAYALTLTRE 360
299 SHQNRDFDMRTTFDDSLVIDNPEYAVTVFVNHDTQSGQALSRVEDWFKPLAYGLTLRHQ 358
361 QGYPSVFYGDYGIPT-THGVPAMRSKIDPILAEAROKYAVGKNDYLDHNIIGWTREGNT 419
359 QGTPLCFYGDYGIQGEFGQCFKEVIDKMAELRQNYVEGKQVDFTTHSNCIGWTCGLGDE 418
420 AHPNSGLATIMSDGAGSKWFMVGRNKAGQVMSDITNGTGTVTINADGWNFSVNGSV 479
419 EH-NSCLAVVLINGDQGWKMEVGEIYAGKTFVDYLGENCEQEVVIGDGDGDFLVBESASI 477
480 SIWVVK 485
478 SAWVPK 483

RESULT 15
Q8DT08 PRELIMINARY; PRT; 486 AA.
AC Q8DT08;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AB014990; AAN59233.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF001128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1. Complete proteome.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;

Query Match 47.6%; Score 1287.5; DB 16; Length 486;
Best Local Similarity 49.2%; Pred. No. 2.9e-74;
Matches 238; Conservative 72; Mismatches 169; Indels 5; Gaps 4;

QY 5 TNGTMMQYFEWYLPNDGNHNRNLNSDASNIKSGKITAVWIPPAWKASQNDVGYGVDLY 64
DB 2 TNETMMQYFEWYLPNDGKHWHLAEDASHLKNIGISKVWMPAPFKGTGSNDVGYGYDLY 61
QY 65 DLGEFNQKGTVRTKYGTRSQLQAATVSLKNGIQVYGDVVMNHKGADATEMVRVAVNP 124
DB 62 DLGEFNQNGTIRTKYGRSDYLNALNKEQETLPIISDIVLNHANGDAKERFQVVKNP 121
QY 125 NNRNOEVTGYTTEAWTRFPDPPGRGNTHSGFKRWYHFGDWDQSRRLNLRNRYKFRGHG 184
DB 122 SNRQEKISEPYEIEGWTGTFDPPGRQGEYDFPKWHYHFTGLDYDALHN-ENGIVMILGDN 180
QY 185 KAW--DWEVDTENGNYDILMYADI DMHDPVVMNELNMGVWYNTLTGLDGRIDAVKH 242
DB 181 KGWASQENIDQENGNYDILMYDDIDFKHPEVQEHLDWVAFLETSGVGGRFLDAIKHD 240
QY 243 YSTRDWINHVSATGKNMFAVEAEKQNDLGAENYLOKTNWNHVSFVDVPLHNLVNA 302
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Db      241 KTFMAQFIRYIREHLKADLYVFGYWKDSHPDITDYLSHSDLOQFDLIDVMLHMSLFEAGQ 300
Qy      303 SGGNYDMRNIFNGTVQRPSPSHAVTFVDNHDSPPEALESEVEWFKPLAYALTITREQ 362
Db      301 KGSDFDLSTILDDSLMKSHDPFAVTFVDNHDSPQQALESVAEWFKPLAYGLILLREQ 360
Qy      363 YPSVFGDYGIP-THGVPMRSDIPLEARQKAYKQNDYLDHNNIIGWTREGNTAH 421
Db      361 IPCVFGDYGYGISGEFAQESFTVLKLLYIRQYHVYGSQEDYFDYANCIGWTCIGDEEH 420
Qy      422 PNSGLATIMSDGAGSKWMFVGRNKAGQVMSDITGNRTGTVINADGWGNSVNGGVS 481
Db      421 PD-GVAVIISNGEANCRRMNGEFNRNKVFVDYLNCTEVLDDQGWGDPFVQESLSA 479
Qy      482 WVNK 485
Db      480 WVNK 483

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